OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:11:10 ; Search time 38 Seconds (without alignments) 25.320 Million cell updates/sec

US-10-047-945-1 54 Perfect score: Title:

1 LKAMDPTPPL 10 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

1102

seq length: 0 seq length: 10 四四四 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	t d	trypsin-modulating	lectin - potato (f	urease (EC 3.5.1.5	peptide-N4- (N-acet	major protein anti	enamelin f - bovin	T-cell receptor be	exotoxin A - Strep	1ph	T-cell receptor be	metallothionein-A	alcohol dehydrogen	triacylglycerol li	hementin (BC 3.4	alpha-gliadin 4Ha	alpha-gliadin 6Ha	acid proteinase li	ATPase R1 subunit	orf 1 rara 5'-regi	Ig H chain V-D-J r	granulocyte-colony	dissimilatory sulf	vitamin D3 26-mono	probable methionin	Ig H chain V-D-J r	T-cell receptor be	e	triacylglycerol li	Ig mu chain J regi
SUMMARIES	ΩI	A36454	S21288	C35389	B59272	B60274	S10783	B30572	A60108	S26508	C30572	151049	871919	PC2171	A61007	A61218	B61218	B37988	D48186	S15594	PH1633	154017	S63491	S15850	B39517	PH1592	PT0664	S18396	PX0030	F33932
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	Score	27	24	21	21	20	20	19	19	19	19	18	18	18	18	17	17	16	16	16	16	15	15	15	15	15	15	15	15	15
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ein - chain	tryptophyllin, bas endoglycosylcerami hypothetical prote T-cell recentor he	leucopyrokinin - M neuropeptide calla ribosomal protein	bradykinin - horn orf dowstream to b hydroxyproline-3-b	bradykinin-like pe Thr-6 bradykinin - bradykinin-like pe	ornitho-kinin - ch
S71299 PT0283	A61081 B39745 S16324 PT0559	A23967 B47393 G35538	S65433 B41983 A43065	A26744 A61057 A60579	B60246
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25.9	255.9 255.9 255.9	25.50	25.5	25.9 25.9 25.9	25.9 9
4 4 4	* * * * *	4 4 4	444	444	14
330		33.0	339 40 41	4 4 4 5 6 4	45

ALIGNMENTS

frypain-modulating oostatic factor - yellow fever mosquito C;Species: Aedes aegypti (yellow fever mosquito) C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004 C;Accession: A35454; A61630 R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F. A5SBB J. 4, 3015-3020, 1990 A;Riele: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi A;Reference number: A36454; MUID:90367888; PMID:2394318

A; Accession: A36454

A;Molecule type: protein A;Residues: 1-10 <BOR>

A;Cross-references: UNIPROT:P19425
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost A;Reference number: A61630 MUID:93357794; PMID:8353526
A;Accession: A61630
A;Accession: A61630
A;Residues: 1-10 <BO2>

A; Note: none of the amino acids is modified

C;Function: A;Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep C;Keywords: hormone

Gape ö Length 10; 1; Indels 7 Score 27; DB 2 Pred. No. 58; 0; Mismatches 50.0%; 4; Conservative Ouery Match Best Local Similarity Matches

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2 DPAPP 6 셤

5 DPTPP 9

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RESULT 2

C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S21288
R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
B;Ochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizatio
A;Reference numbers: S21288; MUID:92272683; PMID:1590771
A;Accession: S21288
A;Molecule type: protein
A;Residues: 1-8 «MIL»
A;Cross-references: UNIPROT:07M1V6
A;Cross-references: UNIPROT:07M1V6
A;Experimental source: var. Ulster Sceptre.
C;Function:

A, Description: may be involved in defence mechanism of the plant

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A; Reference number: A60274; MUID: 91099989; PMID: 1898899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein
                                                                                                                                                    37.0%;
75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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                          A;Accession: B60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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Best Local Similarity
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Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A,Title: Isolation and partial characterization of major protein antigens in the culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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C.Species: Prunus dulcis var. sativa (sweet almond)
C.Species: Prunus dulcis var. sativa
C.Accession: B5927
A.Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Blochem. 252, 118-123, 1998
A.Fitle: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl) asparagine amidase A.Reference number: A5972; MUD:98181894; PMID:9523720
A.Accession: B59272
A.Accession: B59272
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1110 ALIT>
A.Kesidues: 110 ALIT>
A.Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain
N.Alternate names: peptide N-nluchaidase
                                                                                                                                                                                                                                                                                                                     urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Species: Morganella morganii
C;Dete: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C3538
B;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
C;Accession: C35389
A;Hitle: Morganella morganii urease: purification, characterization, and isolation of shiftle: Morganella morganii urease: purification, characterization, and isolation of shiftle: Morganella morganii urease: purification, characterization, and isolation of shiftle: Morganella morganii urease: purification, characterization, and isolation of shiftle: Morganella morganii urease: purification, characterization, and isolation of shiftle: A;Nosecule type: protein
A;Nosecule type: protein
A;Nosecule type: UVIPROT:P17339
C;Keywords: hydrolase
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C, Date: 11-Dec_1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
                                                                                                        Gaps
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                    h Similarity 57.1%; Score 24; DB 2; Length 8; Similarity 57.1%; Pred. No. 2.88+05; 4; Conservative 1; Mismatches 2. Tmann
  C; Keywords: hydroxyproline; lectin
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity
                                                                        Local Similarity
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ASTPSPP 8
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C'Accession: $10783 - 2. C'Accession: $10783 - 2. C'Accession: $10783 - 2. C'Accession: $101mchr. B.; Glimcher, M.J. Bur. J. Biochem. 191, 47-56, 1990 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu. A;Reference nunber: $10780; MUID:90336641; PMID:2379503 A;Accession: $10783 A;Moleçule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Williams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
ArTitle: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz
A;Reference number: A30563; MUID:89110038; PMID:2563271
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                                                                                                                                                                                                                                                                                                                              enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Streptococcus pyogenes
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60108
R;Schlievert, P.M.; Gray, E.D.
Infect. Immun. 57, 1865-1867, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor beta chain C region (CRTB29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr.1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C;Accession: B30572
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment) N,Alternate names: blastogen A; scarlet fever toxin
                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.2%; Score 19; DB 2; Length 9; 100.0%; Pred. No. 2.8e+05; ative 0; Mismatches 0; Indels
   Length 5;
Score 20; DB 2; I
Pred. No. 2.8e+05;
0; Mismatches 1;
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75.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 1;
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2005

05:57:52

Tue May 31

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Gaps

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alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: S11919
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim. Biophys. Acta 1296, 41-46, 1996
A;Title: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol de A;Reference number: S71919; MUID:96150418; PMID:8765227
A;Accession: S71919
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragm Cispecies: Rhizopus niveus
Cispecies: Rhizopus niveus
Cispecies: 
                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 cOLS>
A;Residues: 1-6 cOLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
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C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%; Score 18; DB 2; Length 4; ilarity 100.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 0; Indels
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A;Note: the source is designated Ctenopharyngodon idellus
C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; Score 18; DB 2; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e+03;
tive 0; Mismatches 0;
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Best Local Similarity 100...
Lag 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Collagen alpha 2(VI) chain - bovine (fragment)
C;Decise: Bos primidsenius taurus (cattle)
C;Decise: Bos primidsenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S26508
R;Jander, R.; Rautenberg, J.; Glanville, R.W.
R;Jander, R.; Rautenberg, J.; Glanville, R.W.
Bur. J. Biochem. 133, 39-46, 1983
A;Title: Further characterization of the three polypeptide chains of bovine and human sh
A;Reference number: S26506; MUID:83209648; PMID:6852033
A;Accession: S26508
A;Accession: S26508
A;Status: preliminary
A;Wolecule type: protein
A;Residues: 1-9-43AN>
A;Cross-references: UNIPROT:Q7M2M9
C;Keywords: hydroxyproline
F;7/Modified site: hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
(230572)
T-call receptor beta chain C region (CRTB49) - rat (fragment)
(5,5pedies: Rattus norvegicus (Norway rat)
(5,5pedies: Rattus (R. 1889)
(7,5pedies: Rattus (R. 1889)
(7,5pedies
A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast A;Reference number: A60108; MUID:89254013; PMID:2498210
A;Accession: A60108
A;Molecule type: protein
A;Residues: 1-9 <SCH>
A;Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNIEC;Keywords: exotoxin
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metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
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Best Local Similarity 75.0
Matches 3; Conservative
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Length 8;

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Length 10;

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Alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C,Species: Haynaldia villosa, Dasypyrum villosum
C,Species: Haynaldia villosa, Dasypyrum villosum
C,Accession: A61218
R,Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.
Blochem. Genet. 29, 207-211, 1991
B,Ochem. Genet. 29, 207-211, 1991
A,Afitle: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald A,Reference number: A61218; MUID:91315394; PMID:1859356
A,Accession: A61218
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-10 <a href="https://www.numbro.com/">www.numbro.com/</a>
A,Residues: 1-10 <a href="https://www.numbro.com/">ww.numbro.com/</a>
A,Status: preliminary
A,Grass-references: UNIPROT:Q7M1F7
C;Keywords: seed; storage protein
hementin (EC 3.4,...) - Amazon leech (fragment)
C;Species: Haementeria ghilianii (Amazon leech)
C;Species: Haementeria ghilianii (Amazon leech)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61007
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 355-369, 1990
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from A;Reference number: A61007; MUID:90256973; PMID:2187898
A;Accession: A61007
A;Mesidues: 1-10 <SWA>
A;Cossion: A61007
A;Residues: 1-10 <SWA>
A;Cross-references: UNIPROT:Q7M3P9
C;Keywords: anticoagulant; hydrolase; saliva
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31.5%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels
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Search completed: May 26, 2005, 19:23:37 Job time : 41 secs

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carassius c ctenopharyn haementeria eurypharynx glycine max influenza a cryptococcu staphylococ

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haynaldia v neurospora

polyomaviru

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
"Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut.";
FASEB J. 4:3015-3020(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development.
- DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and stops at 56 hrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Vero beach; TISSUE=Ovary;
MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=83556; DOI=10.1016/0965-1748(93)90044-S;
MASS Spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
Insect Biochem. Mol. Biol. 23:703-712(1993).
-! FUNCTION: Has an oostatic activity, Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
22-OCT-2004 (Rel. 45, Last annotation update)
Trypsin-modulating oostatic factor (TWOP) (OOSH).
Trypsin-modulating oostatic factor (TWOP) (OOSH).
Badéas aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
        0990x5 F
0990x9 F
060x69 C
070x399 h
076mml e
076mml e
089805 G
084140 i
084140 i
08412 c
070x12 e
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YD -> DY (in TMOF(B)).
236D0A7777776DC7 CRC64;
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0; Mismatches
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Direct protein sequencing; Hormone.
DOMAIN 3 10 Poly-P
                     Q9Q0X9
Q6UA69
Q7LZ46
Q7M3P9
Q76MM1
Q9S905
Q8VHM9
Q84140
Q64712
Q70T12
Q77XA62
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90367888; PubMed=2394318
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Vero beach; TISSUE=Ovary;
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 Query Match
Best Local Similarity
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P19425;
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SEQUENCE.
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Q7M1V6;
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Q7M1V6
ID Q7M1
AC Q7M1
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                                                                            May 26, 2005, 19:07:01; Search time 166 Seconds (without alignments) 30.848 Million cell updates/sec
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Q99193
P17339
Q67bk2
P38642
Q89642
Q7m2m9
Q7m2m9
P40930
Q81v76
Q81v76
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Q9q0w9
Q9q0x1
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Q76mk5
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           GenCore version (c) 1993 - 2005
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Q6SP94
Q99193
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Q67BK2
UF04_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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54
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Match Length
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seq length: 10
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Score

Result

 3

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Gaps

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25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A small
chain (BC 3.5.1.52) (PNGase A subunit B) (Glycopeptide N-glycosidase)
(N-glycanase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Borodin A.M., Danilkoyich A.V., Allikmets R.L., Rostapshov V.M., Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;

"Nucleotide sequence of the rpoB gene coding for the beta-subunit of RNA polymerase in Pseudomonas putida.";

Dokl. Biochem. 302:1261-1265 (1988).

BMBL; X15849; CAA33847.1; -.
                                                                                                                                                                                                                                     STRAIN=CC-2290;
MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
                                                                                                                                                                                                                                                                                                              "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
Eukaryotic Cell 2:362-379(2003).
EMBL; AY454155; AAR20844.1; -.
                                                                                                                Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                   Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A., Silflow C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RpoB beta-subunit of RNA polymerase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;
                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER 9 9 SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;
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Pred. No. 1.6e+06;
0; Mismatches 1;
    9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
75.0%;
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75.0%;
                                      (TrEMBLrel. 27, (TrEMBLrel. 27,
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Matches 3; Conservative
    PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=3055
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                                                                                              PF26 (Fragment)
                                        05-JUL-2004
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P81898;
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                                                          Lectin (Fragment).
Solamum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
                                                                                                                                                                                                           Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R., Bolwell G.P.; "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 283:801381.
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44.4%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB046487; BAB87160.1, -..
GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
                    Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATPase subunit 8 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                      8 AA; 771 MW; C37775A771B5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA.
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Mitochondrion.
  Created)
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01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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Matches 3; Conserv
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4 LDPSP 8
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SEQUENCE
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RESULT 3 Q76MK5

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RESULT 4 Q6SP94

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Prunus dulcis (Almond) (Prunus amygdalus)

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Klebsiella pneumoniae.
                                                                                                               (Fragment).
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                                                                                                                                                                                      NCBI_TaxID=573;
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                                                                                                                                                 Plasmid pKP31.
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Matches
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                         RESULT 8
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                                                                                              Altmann F., Paschinger K., Dalik T., Vorauer K.;

"Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A and its N-glycans.";

"Loand its N-glycans.";

Bur. J. Biochem. 252:118-123(1998).

-!- CATALYTIC ACTIVITY: Hydrolysis of an N(4)-(acetyl-beta-D-glucosaminyl)asparagine residue in which the N-acetyl-D-glucosaminylamine residue may be further glycosylated, to yield a glucosamine and an aspartic residue.
                                                                                                                                                                                                                                     deglycosylation.
-!- MASS SPECTROMETRY: MW=21247; METHOD=MALDI; RANGE=1-10; NOTE=Ref.1.
PIR; B59272; B59272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
NCBL TaxID=3755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu L.-T., Nicholson B., Jones B.D., Lynch M.J., Mobley H.L.T., "Morganella morganii urease: purification, characterization, and insolation of gene sequences.", J. Bacteriol. 172:3073-3080 (1990).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBUNIT: (Alpha, beta, gamma) (3) (89 similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the urease gamma subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Morganella.
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                                                                                                                                                                                                              SUBUNIT: Heterodimer of a large and a small chain. PTM: Is highly glycosylated and is resistant against self-
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Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                            Score 21; DB 1; Length 10;
Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                   10 AA; 1149 MW; 863278CAA1E73771 CRC64;
                                                                                                                                                                                                                                                                          Direct protein sequencing; Glycoprotein; Hydrolase.
NON TER 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA
                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                         SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morganella morganii (Proteus morganii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct protein sequencing, Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Urease 6 kDa subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDLINE=90264298; PubMed=2345135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%;
                                                                                                                                                                                                                                                                                                                           38.9%;
Similarity 75.0%;
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
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EPTP 4
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                                                                                                                                                                                                                                                                                                                                                                             5 DPTP 8
                                                                                      PubMed=9523720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ureA;
                                                                         SEOUENCE,
                                                                                                                                                                                                                                                                                                   SEQUENCE
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URE3_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URE3
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Fernandez-Burriel M., Rodriguez-Quinones F., Alonso R.;

"A sull-type integron with a gene cassette for aac(6')-1b, fused in 5'
with a partially deleted gene-cassette DNA region of unknown origin.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY370764; AAR18813.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Michter L.L., He C., Selkirk J.K.;
Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.0, its MM is: 46 kba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
NCBI_TaxID=10090;
                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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01-0CT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (P46) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.9%; Score 21; DB 2; Lengtu ...
Pred. No. 4.3e+03; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
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10 AA; 1026 MW; 9B8F5E376DC1ADC1 CRC64;
                                                                         Last sequence update)
Last annotation update)
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75.0%; Pred. No. 1.6e+06;
10 AA.
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                                                Created)
PRT;
                                              Local Similarity 57.1%;
nes 4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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PRELIMINARY;
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Gaps

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SEQUENCE.
MEDLINE-83209648; PubMed=6852033;
MEDLINE-83209648; PubMed=6852033;
Jander R., Rautenberg J., Glanville R.W.;
Further characterization of the three polypeptide chains of bovine and human short-chain collagen (intima collagen).";
Eur. J. Biochem. 133:39-46(1983).
PIR; 226508; S26508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel FWRFamide-like neuropeptides from the eyestalk of the giant
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE=Ref.l.
-!- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND MASS SPECTROMETRY.
TISSUB=Eyestalk;
Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,
Sithigorngul W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UHA3 HUMAN STANDARD; PRT; 10 AA.
P40930;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-UffL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of heart (Spot 7513) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            freshwater prawn Macrobrachium rosenbergii.";
Comp. Biochem. Physiol. 1208:587-595(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI; RANGE=1-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide-like neuropeptide FLPS (DRTPALALREF-amide).
Macrobrachium rosenbergii (Giant fresh water prawn).
Bukaryota, Metazoa, Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
Palaemonoidea; Palaemonidae; Macrobrachium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 10;
Pred. No. 9.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   Score 19; DB 2; Lengtn >;
Pred. No. 1.68+06;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.

GO; 0007218; P:neuropeptide signaling pathway; TAE
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 10 10 Phenylalanine amide.
SEQÜENCE 10 AA; 1244 MW; 9AIAS334072DC771 CRC64;
                                                                                                                                                                                                                                                                 9 AA; 876 MW; 681467776867605B CRC64;
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                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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75.0%;
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es 3; Conserv
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Best Local Similarity
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                                                            NCBI_TaxID=9913;
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SEQUENCE
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UHA3_HUMAN
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                                                                                                                                                                                                                                                                                   Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.,
"Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
insect cells.";
Shi Yan Sheng Wu Xue Bao 28:283-290(1995).
EMBL; S80660; AABSO710.1; -.
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Luteinizing hormone/chorionic gonadotropin receptor homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US7303; AAB17863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 20; DB 2; Length 10;
50.0%; Pred. No. 6.4e+03;
tive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;
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Last annotation update)
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Last annotation update)
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NCBI_TaxID=11676;
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Pred. No. 6.4e+03;
0; Mismatches 1;
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     10 AA.
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01-MAR-2004 (TrEMBLrel. 26, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last amno
Collagen alpha 2(VI) chain (Fragment)
Bos taurus (Bovine).
                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=96147985; PubMed=8571710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%;
75.0%;
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       PRELIMINARY:
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Name=tat;
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Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Chorion; Receptor.
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PIPP 5
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                                                                                                                        Fragment).
                                                                                                                                         Rattus sp.
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STRAIN=TYLCV-IB;
Wernecke M.E., Roye M.E, McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
Wernecke M.E., Roye M.E, McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
Wennetted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U84397; AAB47965.1; -.
NON_TER 10
SEQUENCE 10 AA; 1058 MW; 25FF98BSA775ASA7 CRC64;
                                                                                                                                                                                                                                                                          Gaps
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                                                                                        TISSUB=Heart;
MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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0
                                                                                                                                                                                                                                             35.2%; Score 19; DB 1; Length 10; 60.0%; Pred. No. 9.5e+03; tive 2; Mismatches 0; Indels
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Pred. No. 9.5e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2 protein (Fragment).
Tomato yellow leaf curl virus (TYLCV).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
                                                                                                                                                                                                                                                                                                                                                                                         10 AA.
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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1 AVEPT 5
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P90391
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Search completed: May 26, 2005, 19:22:05 Job time : 168 secs

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GenCore version 5.1.6
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protein search, using sw model • OM protein

May 26, 2005, 18:45:04; Search time 158 Seconds (without alignments)
24.479 Million cell updates/sec Run on:

US-10-047-945-1 54

1 LKAMDPTPPL 10 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

465227 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 10 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:* geneseqp2004s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

;		de (SUMMARIES		
ult No.	Score	Query Match	Query Match Length DB	DB	ET .	Description	E
	54	100.0	10	7	AAW53843	Aaw53843 N	N-terminu
~	54	100.0	10	7	ABB80222	Abb80222 Sy	Synthetic
m	20	95.6	0	7	ABB80227	Abb80227 Sy	Synthetic
4.	43	9.6	ω	7	ABB80228	Abb80228 Sy	Synthetic
2	30	55.6	9	4	AAB68473	Aab68473 M	Mutated p
9	30	55.6	80	ß	ABB78481	Abb78481 Gu	Gum arabi
7	30	55.6	10	ŝ	ABB78478	Abb78478 Gu	Gum arabi
œ	28	51.9	6	~	AAY47988	Aay47988 In	Immunogen
6	28	51.9	0,	m	AAY86825	-	Telomeras
0	28	51.9	თ	ო	AAY86735		Telomeras
٦.	28	51.9	6	8	ADK07609	Adk07609 He	Hepatitis
Ŋ	28	51.9	7	~	AAR61547	Aar61547 Pe	eptide f
e,	28	51.9	10	~	AAR93336	Aar93336 YE	YES prote
4	28	51.9	10	~	AAY48003	Aay48003 In	Immunogen
'n	28	51.9	10	œ	ADE97778	Ade97778 In	Immunogen
بو	27	50.0	9	~	AAR56874	Aar56874 Oc	Oostatic
۲.	27	20.0	9	~	AAR63465	Aar63465 T	Trypsin M
8 0	27	50.0	9	~	AAR80074	Aar80074 P2	P2 analog
o,	27	20.0	9	~	AAW19715	Aaw19715 Di	Digestion
20	27	50.0	9	~	AAW69749	Aaw69749 Di	Digestion
21	. 27	50.0	9	m	AAB37945	Aab37945 Tr	Trypsin m
22	27	50.0	9	4	AAB30661	-	Trypsin m
m	27	50.0	•	9	ABP58325	Abp58325 Tr	Trypsin m
24	27	50.0	9	7	ADC35474	-	Trypsin m
D.	27	50.0	9	7	ADD10251	Add10251 Mc	Mosquito

Aar56875 Costatic Aar63466 Trypsin M Aar80075 P3 analog Aaw19716 Digestion Aab37946 Trypsin m Abp58326 Trypsin m Adc3475 Trypsin m Adc36475 Trypsin m Adc36475 Trypsin m Adc1025 Mosquito Aar56873 Costatic Aar56873 Costatic Aar56873 Costatic Aar56873 Costatic Aar61075 Digestion Aaw49717 Digestion Aaw45959 Expide # Aar3047 Trypsin M Aar8073 P4 analog Aaw19717 Digestion Aaw45959 Expide #	Abb30663 Trypsin m Abb508327 Trypsin m Adc35476 Trypsin m
7 2 AAR56875 7 2 AAR63466 7 2 AAW19015 7 2 AAW19016 7 3 AAB30366 7 3 AAB303662 7 4 AAB30662 7 7 ADC35475 7 7 ADC35475 8 2 AAR63467 8 2 AAR6073 8 2 AAW89748 8 2 AAW89748 8 2 AAW89748	14.01
227 227 227 227 227 227 227 227 227 227	0.00
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 4 4 4 1 6 4 በ

ALIGNMENTS

AAW53843 standard; peptide; 10 AA N-terminus of opossum LTNF. 08-JUL-1998 (first entry) AAW53843; AAMS 3843 110 AAMS XX AAWS XX AAWS XX AAWS XX ITNN XX ITNN XX BEBE XX ASS XX BEBE XX ASS XX BEBE XX ASS XX

LINF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.

Didelphis virginiana

US5744449-A.

28-APR-1998.

96US-00657163. 03-JUN-1996; 93US-00058387. 94US-00310340. 10-MAY-1993; 22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV;

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.

Claim 7; Col 11; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LINF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

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Sequence 9 AA;
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snake. Being short it can be synthetically prepared rather than the
current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; ELE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
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                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                       ;
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                                                                                                               Length 10;
                                                                                                               100.0%; Score 54; DB 2; Length 10
100.0%; Pred. No. 0.033;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         ABB80222 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 3; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003; 2003WO-US001044.
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                               1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic LTNF, LT-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-636703/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                       to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003060471-A2
                                                                            Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                               Query Match
Best Local S:
Matches 10;
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                                                                                                                                                                                                                                                                                      RESULT 2
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The sequences given in ABBB0222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine demainse (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid chabetes, autoimmune syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                               Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.9
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                    ;
0
                            100.0%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       ABB80227 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                              (first entry)
                                                 Local Similarity 100.
nes 10; Conservative
                                                                                                           1 LKAMDPTPPL 10
                                                                                                                                           LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                  Synthetic LINF, LT-9.
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Ж. С.
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Sequence 10
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                                  Query Match
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                                                       Best Loca
Matches
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LKAMDPTP

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (IgE), insive growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, clabetes, autoimmune disease (e.g. erythematosus (SLE). Theumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva collecting time before centrifugation to separate serum. Saliva proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.9.
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                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                   ö
Score 50; DB 7; Length 5, Pred. No. 1.88+06;
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         92.6%; Scc.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                          ABB80228 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2003; 2003WO-US001044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic LTNF, LT-8.
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                                                                                                                                                                                             Query Match
Best Local Similarity
9; Conserv?
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                                                                                                                                                               1 LKAMDPTPP
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ABB 8020

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ABB 8
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ABB 8
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ABB 8
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ABB 8
ABB 19B;

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Gaps

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0; Indels

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The present sequence represents a mutated portion of an integrase. The specification describes a method for targeting integration of retrotransposon of Tyl-copia group to desired location on a chromosome. The method uses a modified integrase in a retrotransposon, where the modified integrase contains a coding sequence for a peptide portion which specifically binds to protein bound to the chromosome or to particular nucleic acid sequences on chromosome. The method is useful for targeting integration of a retrotransposon of the Tyl-copia group to a desired location on a chromosome, especially into silent chromatin. The silent chromatin targeting of Ty5 is useful for tagging genes which are affected by aging and for studying oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Targeting integration of retrotransposon or retrovirus into silent chromatin by transforming a cell with modified integrase having a coding sequence for a peptide portion that interacts with chromatin at desired
                                                                                                                                                                            Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
                                                                                                                                                                                                           chromatin;
                                                                                                                                                                                                          Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin; chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB78481 standard; peptide; 8 AA.
                                                                                     AAB68473 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Col 66; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                99US-00232446.
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                                                                                                                                               23-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                      paradoxus
           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-342676/36
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LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MDPTPP 9
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                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                    08-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Voytas DF,
                                                                                                                                                                                                                                                         Synthetic
                                                                                                                   AAB68473;
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Matches
                                                        RESULT 5
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                                                                        AAB6847
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Synthetic

HRGP;

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The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich proteins (RRPs) and arabinoglactan-proteins (AGPs) in plants via recombinant methodologies. Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproteins (including the peptide sequences of gum arabic glycoprotein (GAGP)). ABLS1730 to ABLS1849 and ABR78401 to ABB78544 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic peptide having a human leukocyte antigen binding motif #2599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytocoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                   Nucleic acids and proteins useful for producing hydroxy-proline rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.6%; Score 30; DB 5; Le
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                  Claim 5; Page 121; 326pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 131; 150pp; English
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                   12-APR-2000; 2000US-00547693.
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                                                                                                                                                                                                           glycoproteins in plants.
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                                                                                                                                            WPI; 2002-041307/05
                                                            (UYOH-) UNIV OHIO.
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                                                                                                     Kieliszewski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via recombinant methodologies. Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproteins (including the peptide sequences of gum arabic glycoprotein (GAGP)).

ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used in
                                                            Gum arabic glycoprotein, GAGP; hydroxyproline-rich glycoprotein; repetitive proline-rich protein; RPRP; arabinogalactan protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant, Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids and proteins useful for producing hydroxy-proline rich
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                   Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:168.
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention
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Similarity 100.0%; Pred. No.
5; Conservative 0; Mismatra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoproteins in plants.
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Best Local Similarity
Matches 5; Conserv
                                                            Plant; Gum arabic
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                                                                                                       AGP; plant gum
                                                                                                                                            Acacia senegal
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Synthetic.
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Gaps

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Length 10; 0; Indels ŝ

Southwood

ABB78478;

RESULT 7 ABB78478

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having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allale (i.e. HLA-A subtypes HLA-A.1, Al., A3.2 or A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in antigen in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B cancers in mammals carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynucleoutdes encoding the immunogenic peptides are also useful the immunogenic peptides are also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Telomerase; antigenic peptide; cancer; therapy; human; tumour cell; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
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                                     specifically claimed immunogenic
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Pred. No. 1.8e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful therapeutically and for immunisation as above
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local S
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                   lymphocytes
 melanoma, leukaemias, lymphomas, or biliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein or peptide fragments useful in the treatment and prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and can
             tract carcinomas. They are useful for generating telomerase T lymphocy capable of recognising and destroying tumour cells in a mammal, comprising culturing T lymphocytes obtained from the mammal with the peptides. Telomerase protein is expressed only by tumour cells, hence, other body cells are not targeted or destroyed by telomerase specific cells. Note: This sequence was indexed from WO200002581, which is the first major country equivalent to NO9803141
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Telomerase; antigenic peptide; cancer; therapy; human; tumour cell
malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
telomerase T lymphocyte.
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                                                                                                                                                                                                        3; Indels
                                                                                                                                                                            Length 9;
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Pred. No. 1.8e+06;
                                                                                                                                                                        Score 28; DB 3; Pred. No. 1.8e4
                                                                                                                                                                                                                                                                                                                                                     AAY86735 standard; peptide; 9 AA.
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 malignant
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                                                                                                                                                        Query Match
Best Local Similarity 55.00,
Best Local Similarity 55.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telomerase peptide #150.
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                                                                                                                                                                                                                                       2 KAMDPTPPL
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in mammals
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can

This sequence represents a telomerase peptide of the invention, and obe used in a method for the treatment or prophylaxis of cancer. The sequences are useful in the treatment or prophylaxis of cancer especially, breast, lung, ovarian, cervical, colorectal, prostate or

Claim 12; Page 36; 53pp; English.

Matches

ઠે 엄 RESULT 11 ADK07609

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antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIVI; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MACE-1; melanoma antigen-1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AARS9496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (AAR7129). AAR61547 has an ICS0 of 0.0042 and the sequence occurs at position 2803 in the HCV LORF protein. The peptides of the invention can induce cytcoxic T tymphocytes which can react with target calls. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3 ligand; SH3 binding agent; biased phage library; recognition sequence; src SH3 domain; Paget's disease; restenosis; rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47; p67; complex; chronic myelogenous leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                    Peptide fragment (1.0507) of HCV binds HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 2; I
Pred. No. 5.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein tyrosine kinase derived peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 109; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR93336 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                    93US-00027146.
93US-00073205.
93US-00159184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                  94WO-US002353,
11-MAY-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-302678/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTE-) CYTEL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DPTPPL 10
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DPTTPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                    04-MAR-1994;
                                                                                                                                                                                                                                                                       WO9420127-A1
                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1993;
                                                                                                                                                                                                                                                                                                              15-SEP-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reading frame of a pathogenic virus, where the polypoptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypoptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel polypeptide encoded by an alternative
    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; epitope peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus CTL epitope peptide of the
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Indels
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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ص
                                                                                                                                                                                                                                                                                         Hepatitis C virus CTL epitope peptide #5439
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR61547 standard; peptide; 10 AA.
                                                                                                                                                                       ADK07609 standard; peptide; 9 AA.
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  1,
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002AT-00001124
                                                                                                                                                                                                                                                   (first entry)
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                      2 KAMDPTPPL 10
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1 RAODPPPEL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-169243/16
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PTPPM 8
                                                                                                                                                                                                                                                                                                                                                                      HLA-allele; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004011650-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
                                                                                                                                                                                                                                                     06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                               ADK07609;
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Gaps

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RESULT 12 AAR61547

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Southwood S;

Grey HM,

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AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HHA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A3.2 or A24.1 or HLA-B or C) and induce a cytocoxic T call response against the antigen from which the peptide is derived. Cytocoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B cancers in mammals (especially humans) e.g. prostate cancer, hepatitis and C. AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to the peptide e.g. to produce CTLS ex vivo for influsion back into a chickent. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and bove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV; nephrotropic; neuroprotective; antiarthritic; antirheumatic; immunospicessive; dermacological; mascular; nephrotropic; thyromimetic; haemostatic; antithyroid; antianaemic; anabolic; hypertensive; immunogenic peptide composition; immune response; prostate cancer; hepatitis B, hepatitis C; AIDS; renal carcinoma; cervical carcinoma; lymphoma; cytomegalovirus; CW; condlylloma acuminatum; autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis; Sjogren syndrome; scleroderma; polymyositis; dermatomyositis; systemic lupus erthematosus; juvenile rheumatoid arthritis; anybicing spondylitis; myasthenia garvais MG; bullous pemphigoid; pemphigus; glomerulonephritis; Goodpasture's syndrome; autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
                                                                                                                                                                                                                                                                       New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 28; DB 2; I
83.3%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                               Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE97778 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 132; 150pp; English
                                                                                                                                                               Sidney J,
     98WO-US005039.
                                                          98WO-US005039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                             (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                 WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                               Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S DPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
     13-MAR-1998;
                                                          13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE97778;
                                                                                                                                                                  Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR93272-342 represent peptides which are SH3

[1gands/SH3 binding agents. They represent a biased phage library which
comprises six random amino acids flanking the tetrapeptide -PPIP which
comprises six random amino acids flanking the tetrapeptide -PPIP which
comprises a recognition sequence for the src SH3 domain. These
sequences were identified using the method of the invention. The method
comprises contacting the SH3 domain with a mixture of peptides under
conditions permitting a ligand to bind to an SH3 domain to form a
complex. Any unbound peptides are removed and the complexed peptide
[1gands are dissociated from the complexes. The selected peptide
complex are dissociated from the complexes. The selected peptide
complex are dissociated from the Complexes. The selected peptide
complex are dissociated from the Complexes. The selected peptide
conditions or the SH3 domain are detected. The isociated SH3 binding
peptides may be used in the disgnosis, prevention and treatment of
conditions or diseases resulting from cellular processes mediated by an
SH3-based interaction. Such diseases include Paget's disease. Other
conditions treatable with these peptides include restenosis, rheumatoid
arthritis, gout and other problems in which an SH3 of neutrophil oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic peptide having a human leukocyte antigen binding motif #2614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte antigen, binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTD; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                     peptide(8) binding specifically to SH3 domains - for interactions mediated by SH3 domains in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.9%; Score 28; DB 2; Length 10; 55.6%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                             Zoller MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                Botfield MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY48003 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              use in inhibiting interaction e.g. osteoporosis and cancer.
                                                                                                          95WO-US003208
                                                                                                                                                            94US-00209835
                                                                                                                                                                                     95US-00369832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1999 (first entry)
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1es 5; Conservative
                                                                                                                                                                                                                                           (ARIA-) ARIAD PHARM INC.
                                                                                                                                                                                                                                                                                                Brugge JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                               WPI; 1995-328231/42.
                                                                                                                                                                                                                                                                                                                                                                                                       Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
WO9524419-A1
                                                                                                          13-MAR-1995;
                                                                                                                                                            11-MAR-1994;
                                                                                                                                                                                     06-JAN-1995;
                                                                                                                                                                                                                                                                                          Rickles RJ,
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                                                  14-SEP-1995
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Matches

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Gaps

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Length 10; 1; Indels idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease; human leukocyte anitgen A2.1; HLA A2.1; immunogenic HLA-A2.1 binding peptide.

16-SEP-1999,

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residues including a first conserved residue at a second position from residues including a first conserved residue at a second position from N-terminus, and a second conserved residue at C-terminal position. The inventive peptide composition is used to elicit an immune response against a desired antigen for preventing, treating or diagnosing capainst a desired antigen for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B, hepatitis C, ADS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus (CWV), and condlylloma acuminatum. It is also used to treat autoimmune associated disorders, e.g. multiple sclerosis, rheumatoid arthritis, Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic lupus erythematosus, juvenile rheumatoid arthritis, ankylosing spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus, glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia, Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic purpura, Grave's disease, and Addison's disease. The invention defines positions within a motif enabling the selection of the peptides, which will bind efficiently to human leukocyte anitgen (HLA) A2.1. This is the constant of an immunogenic HLA-A2.1 binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an immunogenic peptide composition comprising 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide composition for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B and C, Acquired Immunodeficiency Syndrome, and renal carcinoma, includes conserved residues at specified positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9%; Score 28; DB 8; Length 10; 83.3%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Page 25; 38pp; English.
                                                                                                                                                                                      93US-00027146.
93US-00073205.
93US-00159184.
94US-00349177.
                                                                                                                                                                                                                                                                                                                                                                                   Sidney J;
                                                                                                                                              03-APR-2002; 2002US-00116557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-041186/04.
                                                                                                                                                                                                                                                                                                                                                                                   Sette A,
                                                                                                                                                                                                                                                                                             GREY/) GREY H M.
                                                                                                                                                                                                                                                                                                                   (SETT/) SETTE A. (SIDN/) SIDNEY J.
                                                             US2003185822-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 AA;
                                                                                                                                                                                      05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
02-DEC-1994;
                                                                                                       02-OCT-2003
                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                   Grey HM,
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Gaps ö

Search completed: May 26, 2005, 19:19:14 Job time : 161 secs

S DPTPPL 10 ||| || 5 DPTTPL 10

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Sequence 1, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 168, App
Sequence 165, App
Sequence 165, App
Sequence 273, App
Sequence 273, App
Sequence 273, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 26, Appl
                                                                                                                            May 26, 2005, 19:22:12; Search time 136 Seconds (without alignments) 25.366 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: Cgm2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgm2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgm2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
4: /cgm2_6/ptodata/1/pubpaa/USO6 PUBCOMB.pep:*
5: /cgm2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
6: /cgm2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
7: /cgm2_6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
8: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgm2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgm2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgm2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgm2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: /cgm2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgm2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    185832
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-047-945-1
US-10-047-945-6
US-10-047-945-7
US-10-437-708-168
US-10-438-032-168
US-10-418-032-168
US-10-418-032-165
US-08-344-824-273
US-09-758-128-23
US-09-758-128-23
US-09-758-128-25
US-09-758-128-25
US-09-758-128-25
                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       1462099 seqs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                 US-10-047-945-1
54
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Match Length DB
                                                                                                                                                                                                                                                                       1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 10
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739.6
555.6
555.6
550.0
500.0
500.0
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Perfect score:
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                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                   Run on:
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Sequence 20, Appl	23,	26,		20,	23,	26,	29,	9	23	56	53	7,	Sequence 161	Sequence 7, Appli	7	2002,		4159,	47,	Sequence 2002, Ap	4046	4159	52,	74,		Sequence 1619	Sequence 1620	74,	619	74,	Sequence 619, App		
US-09-758-426-20	US-09-758-426-23	US-09-758-426-26	US-09-758-426-29	US-09-758-198-20	US-09-758-198-23	US-09-758-198-26	US-09-758-198-29	US-09-861-661-20	9	-60-	09-861-6	-09-935-430	-10-224-999	-10-277-292	-10 - 280 - 340	ĭ	US-10-149-138-4046	-10-149-138	10-398-104	US-10-149-138-2002	10-149-138	US-10-149-138-4159	10-930-300	US-09-935-430-74	US-09-935-430-619	US-10-224-999A-1619	US-10-224-999A-1620	US-10-277-292-74	-10-277-2	US-10-280-340-74	US-10-280-340-619	ST.TGNMENTS	ALL GIVIDLA LO
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50.0			50.0								50.0									50.0						50.0		50.0		50.0	ö		
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14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	53	30	31	32	33	34	35	36	37	38	39	40,	41	42	43	44	45		

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RESULT 1

1 Sequence 1, Application US/10047945

1 Sequence 1, Application US/10047945

2 Sequence 1, Application No. US2003015755A1

3 GENERAL INPORMATION:

4 APPLICANT: LIPPS, FREDERICK W.

5 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

5 FILE REFERENCE: FWLPAT015US

5 CURRENT PILING DATE: 2002-01-14

5 FRIOR APPLICATION NUMBER: US/10/047,945

5 CURRENT PILING DATE:

6 NUMBER OF SEQ ID NOS: 7

7 SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

7 SEQ ID NO 1

7 TYPE: FRY

8 SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

9 SEQ ID NO 1

7 TYPE: FRY

9 ORGANISM: Artificial Sequence

10 TYPE: NAME/KEY:

10 CCATION:

10 CCATION:

10 CHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM

10 CTHER INFORMATION: US 5,576,297.

10 CUETY MATCH

10 COASINATION: US 0.007;

MATCHES 10; CONSELVATIVE 0; Mismatches 0; Indels 0; Gaps
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LKAMDPTPPL 10

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TYPE: PRT
ORGANISM: Artificial Sequence
US20040009555A1
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OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-418-032-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-437-708-168
                                                                                                                                                                                                                                                       LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corresponds to fragment 1-9 of 2 above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/10047945; Publication No. US2003015755541
; CENDEAL INFORMATION:
; APPLICANT: LIPPS, BINLE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: IGE) IMPLICATED DISORDERS;
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS;
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS;
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS;
; TITLE OF INVENTION INVERES: US/10/047,945;
; CURRENT FILING DATE: 2002-01-14
; PRIOR PELICATION NUMBER: US/10/047,945;
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 8
                        Sequence 6, Application US/10047945
Fublication No. US2030127555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1gE) IMPLICATED DISORDERS
TITLE OF INVENTION: (1gE) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US/10/047,945
PRIOR PAPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 6
LENGTH: 9
LENGTH: 9
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1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; L
1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.6%; Score 50; DB 100.0%; Pred. No. 1.3 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%; Score 43; DB 100.0%; Pred. No. 1.3 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 168, Application US/10437708
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTPP 9
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US-10-437-708-168
                    US-10-047-945-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-047-945-6
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US-10-047-945-7
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APPLICANT: Kleliszewski, Marcia
APPLICANT: Kleliszewski, Marcia
TITLE OF INVENTION: Glycoproteins
TITLE OF INVENTION: Glycoproteins
TITLE OF INVENTION: Glycoproteins
TITLE OF INVENTION: Glycoproteins
FILE REPERBNCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US/09/547,693
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 168 Application US/10418032

Sequence 168 Application US/10418032

Publication No. US20050074838A1

GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia J.

TITLE OF INVENTION: Synchetic Genes for Plant Gums and Other Hydroxyproline-Rich

TITLE OF INVENTION: Glycoproteins

FILE REFERENCE: OHU-07775

CURRENT APPLICATION NUMBER: US/10/418,032

CURRENT FILING DATE: 2003-04-16

NUMBER OF SEQ ID NOS: 274

SOFTWARE: Patentin version 3.2

SEQ ID NO 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (3)...(4)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (3)...(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline
US-10-418-032-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(1) OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%; Score 30; DB 15; Length 8; 100.0%; Pred. No. 1.3e+06; cive 0; Mismatches 0; Indels
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Gaps
                                                                                             .; LOCATION: (5). (6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline. US-10-418-032-165
                                                                                                                                                                                                                                            Gaps
LOCATION: (3)...(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273, Application US/08344824

Sequence 273, Application US/08344824

Publication No. US20030152580A1

GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: One Market Plaza, Steuart Street Tower, 20th
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                        Query Match
55.6%; Score 30; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Ploppy disk
COMPUTER: Plan Pro-Compatible
COMPUTER: Plan Pro-Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/248,634
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 14137-80-1
TELEPHONE: (415) 542-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 28; DB 8; I
83.3%; Pred. No. 1.3e+06;
tive 0; Mismatches 1;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                      NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
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Best Local Similarity
Matches 5; Conserv
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US-08-344-824-381
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                                                                                     Sequence 165, Application US/10437708

Sequence 165, Application US/10437708

Sequence 165, Application US/10437708

PUBLicano No. US20040009555A1

GENERAL INFORMATION:
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REPERENCE: OHU-04089

CURRENT APPLICATION NUMBER: US/10/437,708

CURRENT PILING DATE: 2003-05-14

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 236

SEQ ID NO 165

LENGTH: 10
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TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins
FILLE REFERENCE: OHU-07775
CURRENT APPLICATION NUMBER: US/10/418,032
CURRENT APPLICATION NUMBER: US/10/418,032
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165, Application US/10418032; Publication No. US20050074838A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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3 PTPPL 7
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NAME/KEY: SITE
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LENGTH: 10
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US-09-758-128-23

i Sequence 23, Application US/09758128

i Sequence 23, Application US/09758128

i Detent No. US20020107187A1

i GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: WESTERROOK, Simon L.

TITLE OF INVENTION: MODULAFING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US/09/758,128

PRIOR APPLICATION NUMBER: 09/194,218

PRIOR APPLICATION NUMBER: AU PN9990

PRIOR PELING DATE: 1996-02-05

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTIN OF THE NOS: 58

SEQ ID NO 23

LENTH: 8

LENTH: 8

LENTH: 8

LENTH: 8
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Sequence 26, Application US/09758128

Sequence 26, Application US/09758128

Sequence 100. US20020107187A1

SERRATY INFORMATION:

APPLICANT: GERRATY, No. US20020107187Alman L.

APPLICANT: GERRATY, No. US20020107187Alman L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF;

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 58
                                                                                                  Score 27; DB 9; Length 8; Pred. No. 1.3e+06; 1; Mismatches 2; Indels
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Pred. No. 1.3e+06;
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5
Local 5; Conservative
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; TYPE: PRT
; ORGANISM: Bovine
US-09-758-128-20
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US-09-758-128-20
is Sequence 20. Application US/09758128
is Patent No. US20020107187A1
is GENERAL INFORMATION:
is APPLICANT: KINGSTON, David J.
is APPLICANT: WESTBROOK, Simon L.
is APPLICANT: WESTBROOK, Simon L.
is TILLE OF INVENTION: WOULDATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
is TILLE OF INVENTION: WOULDATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
is TILLE OF INVENTION: WOULDATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
is TILLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
is TILLE OF INVENTION: DATE: 1090-02-05
is PRIOR APPLICATION NUMBER: 09/194,218
is PRIOR PILING DATE: 1996-05-22
is NUMBER OF SEQ ID NOS: 58
is SOFTWARE: PATENTIN VET: 2.0
is SEQ ID NO 20
is LENGTH: 8
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0
          Publication No. US20030152580Al
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
GORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Floor
CITY: San Francisco
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTI PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.9%; Score 28; DB 8; Length 10; Best Local Similarity 83.3%; Pred. No. 5.9e+02; Matches 5; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824

FILING DATE: 23-NOV-1994

FILING DATE: 21-NOV-1994

PRICK APPLICATION DATA:

APPLICATION NUMBER: US/08/634

FILING DATE: 21-JUL-1994

ATOONEY/AGENT INFORMATION:

NAME: BASTIAN, Kevin I

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

RELERANCE/DOCKET NUMBER: 34,774

RELERANCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-344-824-381
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STRANDEDNESS: si
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Search completed: May 26, 2005, 19:35:47 Job time: 188 secs
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Matches 5; Conservative
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1 AISPTPAL
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## APPLICANT: WESTRATY, No. US20020169116Alman L.

## APPLICANT: WESTRATY, No. US20040169116Alman L.

## APPLICANT: WESTRATY, No. US20040169116Alman L.

## APPLICANT: US2004016Alman L.

## APPLICAN
                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09758128

Patent No. US20020107187A1

GENERAL INFORMATION:

APPLICANT: GENERATY, No. US20020107187A1man L.

APPLICANT: GENERATY, No. US20020107187A1man L.

APPLICANT: GENERATY, No. US20020107187A1man L.

TITLE OF INVENTION: WODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTIN VET. 2.0

SOFTWARE: PATENTIN VET. 2.0

SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 62.5°
"--rhes 5; Conservative
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                                                                                                              3 AMDPTPPL 10
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1 AISPTPAL 8
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-29
                                                                                                                                                                                                                                                                                   RESULT 13
US-09-758-128-29
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LENGTH: 8
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Sequence 23 Application US/09758426
; Sequence 23 Application US/09758426
; Patent No. US2020169116A1
; GENERAL INFORMATION:
    APPLICANT: KINGSTON, David J.
    APPLICANT: GENERAY, No. US2020169116A1man L.
    APPLICANT: GENERAY, No. US2020169116A1man L.
    APPLICANT: GENERAY, NO. US2020169116A1man L.
    TITLE OF INVENTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION: OPPLICANTION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR PLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR PLICATION NUMBER: AU PN9990
; NUMBER OF SEQ ID NOS: 58
; SOFTWARR: Patentin Ver: 2.0
; SECTUANTE: PATENTIN VER: 2.0
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62.5%; Pred. No. 1.3e+06;
tive 1; Mismatches 2.
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TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINBAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77401
                                                                                                                                                                                                                                                                                                                                                                  US-08-657-163A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                        May 26, 2005, 19:08:54 ; Search time 41 Seconds (without alignments) 18.207 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
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Sequence 1
Sequence 1
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-2446B-24
US-09-547-693-168
US-09-547-693-168
US-09-591-25
US-08-468-596-2
US-09-295-96B-12
US-09-295-96B-12
US-09-295-96B-12
US-09-295-96B-12
US-09-295-96B-13
US-09-295-96B-13
US-09-295-96B-13
US-09-595-96B-13
US-09-551-73RE-13
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-551-737C-17
US-09-295-924B-4
                                                                                                                                                                                                                                                                 513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                           US-10-047-945-1
54
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Match Length DB
                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 10
                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                     Scoring table:
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Maximum DB E
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                                                                                           Run on:
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Sequence 8, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 7, Appli
Sequence 8, Appli
Sequence 33, Appl
Sequence 103, App
Sequence 14, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 86, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/08657163A; Patent No. 5744449; GENERAL INFORMATION; Patent No. 5744449; GENERAL INFORMATION; TITLE OF INVENTION: SYNTHETIC LINES AND FREDERICK W. LIPPS; TITLE OF INVENTION: SYNTHETIC LINES AND THEIR; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION; NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: BINIE V. LIPPS; STREET: 4509 MIMOSA DR. CITY: BELLAIRE STATE: TEXAS.

COUNTRY: USA
US-09-551-738B-14

US-09-295-996B-8

US-09-295-996B-11

US-09-251-737C-11

US-09-551-738B-8

US-08-895-59-40

US-08-895-59-40

US-08-841-943-33

US-08-841-943-33

US-08-841-943-33

US-08-841-943-86

US-09-822-270-9

US-08-340-283-86

US-08-340-333-047-12

US-08-340-343-047-12

US-07-972-032-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.5" FLOPPY DISK, 1.44 MB
COMPUTER: 13.6" FLOPPY DISK, 1.44 MB
COMPUTER: 13.6" MS-DOS 5.0/MINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: 2.4
PRIOR APPLICATION DATA:
APPLICATION WUMBER: 08/310,340
FILING DATE: 2.2 SEPTEMBER 1994
CLASSIFTCATION: 2.4
APPLICATION NUMBER: 08/310,340
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
ANAME: ACADED SON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FWL-PAT-US-011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FM.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
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55.6%; Score 30; DB 4;
                                100.0%; Pred. ...
                                                                                                                                                                                                                          ; Sequence 165, Application US/09547693
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                   Query Match 55.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.6
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                             6 PTPPL 10
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                                                                                                                                                                                      RESULT 4
US-09-547-693-165
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 165
LENGIH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (3)..(4)
; CTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:mxutant peptide; OTHER INFORMATION: sequence
US-09-232-446B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (1). (1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
NAME/KEY: SITE
                                                                                                                                                                                                                                       US-09-232-446B-24

Sequence 24, Application US/09232446B

Sequence 24, Application US/09232446B

Sequence 24, Application US/09232446B

SEMERAL INFORMATION:

APPLICANT: Voytas, Daniel F.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Transposable Element Protein that Directs DNA

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

FILE REFERENCE: 2-98
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                                                         Length 10;
                                        Score 54; DB 1; Length 10
Pred. No. 0.0043;
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                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/232,446B;
CURRENT APPLICATION NUMBER: US/09/232,446B;
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1998-01-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 24
LENGTH: 6
                                                                                          0; Mismatches
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CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
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                                                       100.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial/Unknown
 SYNTHETIC
                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.6
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                  1 LKAMDPTPPL 10
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1 LDPSPP 6
ORIGINAL SOURCE:
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SEQ ID NO 168
LENGTH: 8
       ; US-08-657-163A-2
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Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliezewski, Marcia
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
NAME/KEY: SITE
LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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Length 8;
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Patent No. 5358934

GENERAL INFORMATION

APPLICANT: Borovsky, Dov

APPLICANT: Carlson, David A.

ITILE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                    4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%; Score 30; DB 100.0%; Pred. No. 43; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
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us-10-047-945-1.closed.rai

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Gaps
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                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08468596
Fatent No. 5629196
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: Of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STREET: PL
                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
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ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 0.5-UN-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1997
ATTORNEY/AGRNT INFORMATION:
NAME: SAIWANCHIK, DAVIG R.
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/ScS-127
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
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Pred. No. 4.1e+05;
0; Mismatches 1;
                                                                                             Score 27; DB 1; I Pred. No. 4.1e+05; 0; Mismatches 1;
                                                                                             50.0%;
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80.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0 Best Local Similarity 80.0 Matches 4; Conservative
                                                                                                                                         4; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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        ; HYPOTHETICAL: N; ANTI-SENSE: NO US-08-271-698-2
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US-09-295-996B-12
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; Sequence 2, Application US/08271698
; Patent No. 5439821
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: Of Pests
; CORRESPONDENCE ADDRESS:
; ADDRESSE: ADDRESSE:
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 1; Length 6; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITATE: 4211 N.W. 41EC SITEEL, SUITE A-1
CITY: Gainesville
STATE: FL
COMPUTER: FL
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPBY disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REPERBUCK/DOCKET NUMBER: US/05/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRHONE: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUIBNER CHARACTERISTICS:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECHONE: 904-375-8100
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6 mills acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-989-290-2
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STRANDEDNESS: single
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Best Local Similarity
4; Conserve
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SEQ ID NO 2
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; Sequence 15, Application US/09551737C
; Patent No. 6566129
; GENERAL INFORMATION:
APPLICANT: Schlesbinger, Sabine M. I.
APPLICANT: Naturelaers, Sabine M. I.
TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
FILE REFREENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US 09/551,737C
; CURRENT FILING DATE: 1099-04-21
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOTOWSKY, Dov
TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
FILE REFERENCE: UF-223
CURRENT APPLICATION WOMBER: US/09/295,846B
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: TMOF peptide US-09-295-846B-15
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Pred. No. 4.1e+05;
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                                                    APPLICANT: BOICO'SKY, DOV
TITLE OF INVENTION: PESTICIDAL PEPTIDES
FILE REFERENCE: UF-230
CURRENT APPLICATION NUMBER: US/09/295, 996B
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 60
SOFWARE: Patentin version 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-295-846B-15; Sequence 15, Application US/09295846B; Patent No. 6562590; GENERAL INFORMATION:
Sequence 12, Application US/09295996B
Patent No. 6413530
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: TMOF peptide US-09-295-996B-12
                                                                                                                                                                                                                                                                                                                                                          50.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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US-09-551-737C-15
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GENERAL INFORMATION:
APPLICANT: BOTOWSKY, DOV
TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
FILE REFERENCE: UP-22441
CURRENT APPLICATION NUMBER: US/09/551,738B
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/296,113
PRIOR FILING DATE: 1999-04-21
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Patent No. 6593299
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Alan, Bernett
APPLICANT: Alan, Bernett
APPLICANT: Dov, Borovski
TITLE ON BOROVSKI
FILE REFERENCE: 4137-120
CURRENT APPLICATION NUMBER: US/09/295,924B
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
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                                                                                                                 Score 27; DB 4; Length 6; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
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OTHER INFORMATION: Truncated TMOF
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, OTHER INFORMATION: TMOF peptide
US-09-551-738B-12
                                   ; FEATURE;
; OTHER INFORMATION: TMOF peptide
US-09-551-737C-15
TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                       50.0%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 6
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 80..
---- 4; Conservative
                                                                                                                   Query Match 50.0
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
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US-09-551-738B-12
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| Patent No. 5629196
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Borovsky, Dov
| TITLE OF INVENTION: Materials and Methods for Control
| TITLE OF INVENTION: Of Pests
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: David R. Saliwanchik
| STREET: 2421 N.W. 41st Street, Suite A-1
| STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 1; Length 7;
                                                                                                                                                           OPERATION SYSTEM: TC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: US/07/989,290
FILING APPLICATION TATA:
APPLICATION NUMBER: US/07/989,290
FILING APPLICATION NUMBER: US/07/989,290
FILING APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTONENT/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/SES-127
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 904-275-8100
TELEFRAK: 904-275-810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 32606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/271,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1e+05;
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0; Mismatches
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APPLICATION NUMBER: US/07/989,290
                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
    Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 DPTPP 9
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US-08-271-698-3
                                                                 32606
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US-08-468-596-3
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                                                                                                                                         RESULT 13
US-07-980-290-3
i Sequence 3, Application US/07989290
i Patent No. 5358934
j GENERAL INFORMATION:
i APPLICANT: Borovsky, Dov
i TITLE OF INVENTION: Materials and Methods for Control
i TITLE OF INVENTION: Of Pests
i TITLE OF SEQUENCES:
i ADDRESSEE: David R. Saliwanchik
i STREET: 2421 N.W. 41st Street, Suite A-1
i CITY:
i CITY: Gainesville
  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
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US-08-271-698-3
Sequence 3, Application US/08271698
Sequence 3, Application US/08271698
Sequence 3, Application US/08271698
Sequence 3, Application US/08271698
SEMERAL INFORMATION:
APPLICANT: Boroveky, Dov.
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES. 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTONREY/AGERT INPORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/POCKET UNBER: 31,794
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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2421 N.W. 41st Street, Suite A-1
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 904-372-5800
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
Matches 4; Conserv
                                          5 DPTPP 9
                                                                                   DPAPP 6
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US-07-989-290-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Matches
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Search completed: May 26, 2005, 19:22:51 Job time : 42 secs

2 DPAPP 6

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

26, 2005, 19:31:54 ; Search time 38 Seconds (without alignments) 37.980 Million cell updates/sec Run on:

US-10-047-945-2 Title: Perfect score:

1 LKAMDPTPPLWIKTE 15 Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

2523 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 15 Minimum I Maximum I Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	27	32.1	7	~	A61081	trvotophyllin, bas
7	27	32.1	10	~	A36454	يد
٣	27	32.1	15	7	A47628	Fc damma receptor
4	25	29.8	13	N	PH1620	Ig H chain V-D-J r
Ŋ	25	29.8	15	~	PD0444	coupling factor 6
9	24	28.6		N	S21288	lectin - potato (f
7	23	27.4		4	A58725	virotoxin - destro
8	23	27.4	1	~	158273	thyroglobulin - ra
σ	23	27.4	7	~	B39109	hypothetical 1.5K
10	23	27.4	1	7	B61457	alpha-glucosidase
11	22	26.2	1	N	G37266	Ig heavy chain C r
12	22	26.2	-	~	D37267	
13	22	26.2	-	7	PT0026	calotropin DI - mu
14	22	26.2	7	ď	PT0037	light harvesting c
15	21	25.0	-	~	C35389	urease (EC 3.5.1.5
16	21	25.0	-	~	B59272	peptide-N4-(N-acet
17	21	25.0	7	N	839030	lysyl-bradykinin -
18	21	25.0	11	Н	XAVIBH	bradykinin-potenti
19	21	25.0	7	7	C59151	protein-tyrosine k
20	21	25.0	7	~	PA0055	protein QF200007 -
21	21	25.0	15	~	A26212	carboxypeptidase B
22	20	23.8		2	B60274	major protein anti
23	20	23.8		~	S10783	enamelin f - bovin
24	20	23.8		7	A39308	qlycine reductase
25	20	23.8		7	878426	52.5K protein - sp
56	20	23.8		Н	JTJG0	tremerogen A-10 -
27	20	23.8		~	PN0663	dystrophin-associa
28	20	23.8	14	~	PH1348	Ig heavy chain DJ
53	20	23.8	14	N	A60158	disaggregatase - M

	ubiquitin thiolest ubiquitin thiolest T-cell recentor be	exotoxin A - Strep collagen alpha 2(V	T-cell receptor be complement C3b rec	TCR gamma V-J regi cell surface glyco	H+-transporting tw protein kinase (EC	Pax-QNR, long form dichloromethane de	serine proteinase
S33801 S33802	S10891 PT0093 B30572	A60108 S26508	C30572 D45900	A49037 A40207	F33160 S12904	B56884 A60929	867918
01 01	0 0 0	00	0 0	~ ~	77	0 0	0
14	15 15 9		11	11	14 14	14 15	15
23.8 23.8	23.8	22.6	22.6 22.6	22.6 22.6	22.6 22.6	22.6	22.6
20 50	700	19	19	19 19	19	19	19
30 31	0 0 0 0 0 4	32 36	37 38	39 40	4142	4 4 4	45

ALIGNMENTS

		- Rohde's leaf fro
		basic
SULT 1	1081	yptophyllin,

tryptophyllin, basic - Rohde's leaf frog C;Species: Phyllomedusa rohdei (Rohde's leaf frog) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C; Accession: A61081
R; Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
R; Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
A; Title: Isolation, structure determination and synthesis of a novel tryptophan-containi A; Reference number: A61081
A; Accession: A61081

A,Molecule type: protein A,Residues: 1-7 <MON> C,Comment: The biological activity of this peptide was not determined.

C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; hydroxyproline; skin
C; Keywoids: amidated carboxyl end; hydroxyproline; experimental
F; J/Modified site: 4-hydroxyproline (Pro) #status experimental

Gaps ; Score 27; DB 2; Length 7; Pred. No. 2.8e+05; 0; Mismatches 1; Indels 32.1%; 80.0%; Query Match
Best Local Similarity 80.0
Matches 4; Conservative

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8 PPLWI 12 PPSWI 6

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trypsin-modulating oostatic factor - yellow fever mosquito C.Species: Aedes aegypti (yellow fever mosquito) C.Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C;Accession: A36454; A61630 —
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A585B J. 4, 3015-3020, 1990
A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi·
A;Reference number: A36454; MUID:90367888; PMID:2394318
A;Accession: A36454

A; Molecule type: protein A; Residues: 1-10 < BOR>

A;Cross-references: UNIPROT:P19425
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost A;Reference number: A61630; MUID:93357794; PMID:8353526

A,Molecule type: protein A,Residues: 1-10 <BO2> A,Note: none of the amino acids is modified C,Function:

A; Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep

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27.4%;
                                                                                   29.8%;
36.4%;
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                                                                                                                             Conservative
                                                                                                                                                                         2 KAMDPTPPLWI 12
                                                                                                                                                                                                  2 KELDPVOKLFV 12
A;Molecule type: protein
A;Residues: 1-15 <KAW>
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
4; Conserve
                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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PH1620
IG Heain V-D-J region (clone B-less 40) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1620
C;Accession: PH1620
C;Accession: D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Accession: PH1620
A;Molecule type: DNA
A;Residues: 1-13 < LNA
A;Residues: 1-13 < LNA
A;Residues: 1-13 < LNA
A;Residues: 1-13 < LNA
C;Keywords: immunoglobulin
                                                                                                                                                                                                                          RESULT 3
A47628
C. Gamma receptor II (CD32) - human (fragments)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: U3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C. Schocession: A7628
R. Warmerdam, P. A. M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.
J. Exp. Med. 172, 19-25, 1990
A. Title: Molecular basis for a polymorphism of human Fcgamma receptor II (CD32).
A. Reference number: A47628; MUID:90293679; PMID:2141627
A. Accession: A47628
A. Molecular type: mRNA
A. Residues: 175 cMAR>
C. Keywords: immunoglobulin receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
C;Accession: PD0444
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. A;Description: Proteome analysis of mouse brain.
A;Reference number: PD0441
A;Contents: Striatum
                                                                                      Gaps
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0
                                       32.1%; Score 27; DB 2; Length 10; 80.0%; Pred. No. 1.8e+02; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.1%; Score 27; DB 2; Length 15; 50.0%; Pred. No. 2.8e+02; Live 0; Mismatches 4; Indels
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                                                                                   4; Conservative
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                             Local Similarity
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                                                                                                                           5 DPTPP 9
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C; Keywords: hormone
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                                         Query Match
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lectin - potato (fragment)
Cispeciaes: Solanum tuberosum (potato)
Cispeciaes: Solanum tuberosum (potato)
Cispeciaes: Solanum tuberosum
A. 213, 1912
A. Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizatio
A. Reference number: S21288; MUD: 92272683; PMID: 1590771
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C;Accession: A58725
R;Faulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A;Reference number: A58725; MUID:6893271; PMID:6893271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: protein
A;Rolecule type: D-4 Mydroxyproline; toxin; unencoded polypeptide
F;1-7/Cross-link: cyclopeptide (Val-Leu) #status experimental
F;1/Modified site: D-serine (SPr) #status experimental
F;4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental
F;6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F;7/Modified site: 4,5-dihydroxyleucine (Leu) #status experimental
                                                                    Gaps
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Length 15;
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Score 25; DB 2; Pred. No. 5.8e+02;
                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-8 <MIL>
A;Cross-references: UNIPROT:Q7M1V6
A;Experimental source: var. Ulster Sceptre
C;Punction:
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C, Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

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Gaps

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R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: G37266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: D37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
A;Title: Heavy and light chain variable region sequences and antibody properties of anti A;Reference number: A38740; MUID:91177923; PMID:1706720
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Phytochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotro
                                                                                                                                                                                                                                                                                                                                              Ig heavy chain C region (Py2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
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C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
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                                           Length 15;
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                                           DB 2; Le
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Pred. No. 1.5e+03;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  j heavy chain C region (Py69) - mouse (fragment)
Species: Mus musculus (house mouse)
                                        27.4%; Score 23; DB 100.0%; Pred. No. 1.2 rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calotropin DI - mudar (fragment)
                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.2
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-14 <BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <RUF>
                                                                                                                                                       7 TPPL 10
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A;Molecule type: mRNA
A;Residues: 1-13 <RUF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 PLW 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: G37266
                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternate names: hypothetical protein 2
Cispecies: hepatitis C virus
A, Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A, Reference number: A39109; MUID:91156678; PMID:1705704
A; Accession: B39109
thyroglobulin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 158273
R;Musti, A.M.; Ursini, V.M.; Avvedimento, E.V.; Zimarino, V.; Di Lauro, R.
Nucleic Acids Res. 15, 8149-8166, 1987
A;Tele: A cell type specific factor recognizes the rat thyroglobulin promoter.
A;Reference number: 158273
A;Reference number: 158273
A;Accession: 158273
A;Accession: IS8273
A;Accession: Yes: DNA
A;Residues: 1-12 - RES>
A;Cross-references: UNIPROT:Q63579; EMBL:X06162; NID:g57368; PIDN:CAA29519.1; PID:g57369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: not compared with conceptual translation
A, Molecule type: mRNA
A, Residues: 1-15 < HANN-
A, Cross-references: GB158406
R, Rumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
Gen. Virol. 73, 1521-1525, 1992
A, Reference number: JQ1584; MUID:92300349; PMID:1318944
A, Accession: JQ1585
A, Accession: JQ1585
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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C;Accession: B61457 N:; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purificatio
A;Accession: B61457
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B61457
alpha-glucosidase (BC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
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Pred. No. 9.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 23; DB 2; Length 15; 80.0%; Pred. No. 1.2e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.
                                                                                                                                                                                                                                                                                                                                                                                                     27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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A; Residues: 1-15 <BAN>
C; Genetics:
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Matches 4; Conserv
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Gaps

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RESULT 15
C35389
C35389
Cyrease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
Cypate: Morganella morganii
Cypate: Morganella morganii
Cypate: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C3538
R;Au. Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Nacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Reference number: A35389; MUD:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 < HUA>
A;Residues: 1-10 < HUA>
A;Residues: 1-10 < HUA>
A;Cypaternces: UNIPROT:P17339
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      light harvesting complex chain III/b, photosystem I - rice (fragment)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Accession: PT0037; PS0205
R;Uchiyama, Y; Tsugita, A.
Bubmitted to JIPID, June 1991
A;Reference number: PS0189
A;Reference property protein
A;Reference control of the protein
A;Reference control of the protein
A;Residues: 1-15 < UCH>
A;Residues: 1-15 < UCH>
A;Cross-references: UNIPROT:Q7MIVI
                                                                                                                                                                        Gaps
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C;Comment: This enzyme is classified as a plant cysteine protease.
C;Keywords: pyroglutamic acid
F;I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                             Query Match 26.2%; Score 22; DB 2; Length 14; Best Local Similarity 50.0%; Pred. No. 1.7e+03; Matches 3; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.2%; Score 22; DB 2; Length 15; Best Local Similarity 50.0%; Pred. No. 1.8e+03; Matches 4; Conservative 1; Mismatches 3; Indels
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PT0037
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Search completed: May 26, 2005, 19:41:22 Job time : 43 secs

1 MQLTPP 6

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on:

May 26, 2005, 19:23:42; Search time 165 Seconds (without alignments) 46.553 Million cell updates/sec

US-10-047-945-2 84

1 LKAMDPTPPLWIKTE 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

6622 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c	pachymedusa	aedes aegyp	o sapien	o sapien	canis famil	acinetobact	lymantria d	s castan	s gracil	solanum tub	drosophila	eurypharynx	homo sapien	rattus norv	human immun	numan immun	clivia mini	numan immun	an immun	numan immun	maripa pani	maripa repe	wilsonia hu	seddera hir	odonellia h	aniseia arg	merremia pe	ipomoea alb	solanum tub	calotropis	solanum tub
Description				1 homo	-	-	• •	1 anas	-		_	_			_	_	_	_	13 human	_		-	-			-	_			_	
Desci	P83455	P19425	Q96qp2	Q9ucr1	Q6x7v1	Q8kz86	P80941	Q9ten1	Q9ten3	Q7m1v6	Q68e52	Q76mk5	Q8ivg8	063579	P12509	P12511	Q8hr43	Q8jdn	Q8jdn	Q8jdm7	Q8maz1	Q8maz3	Q8mb39	Q8mb58	Q8mb77	Q8mb79	Q8mb97	Q8mbe1	043174	P20728	Q9t2g9
aı	TPFY PACDA	TMOF AEDAE	Q96Q <u>P</u> 2	Q9UCR1	Q6X7V1	Q8KZ86	ECDE_LYMDI	Q9TEN1	Q9TEN3	Q7M1V6	Q6SE52	Q76MK5	Q8IVG8	Q63579	TAT HV1W2	TAT_HV1Z8	Q8HR43	ОВЛОМО	Овломз	Фвлрм7	Q8MAZ1	Q8MAZ3	O8MB39 .	Q8MB58	Q8MB77	Q8MB79	Q8MB97	Q8MBE1	Q43174	CALL_CALGI	Q9T2G9
DB	-	Н	~	N	7	~	-	~	~	~	~	~	~	N	Н	ч	~	~	~	7	~	~	~	~	~	~	~	~	~	-	7
Length	7	10	14	11	12	12	13	14	14	80	14	10	11	12	14	14	14	14	14	14	11	11	11	11	11	11	11	11	13	14	15
×α	32.1	32.1	32.1	31.0	29.8	29.8	29.8	29.8	29.8	28.6	28.6	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	27.4	26.2	26.2	26.2	26.2	26.2	26.2		•	26.2	26.2	26.2
Score	27	27	27	26		25	25	25	25	24	24	23	23	23	23	23	23	23	23	23	22	22	22	22	22	22	22	22	22	22	22
Result No.	1	7	m	4	ស	9	7	60	σ	10	11	12	13	14	15	16	17	18		20				24	25	26	27	28		30	31

oryza sativ gossypium h litoria rub homo sapien chlamydomon pseudomonas lepisosteus oncorhynchu prunus dulc morganella klebsiella agkistrodon oreochromis
Q7mlv1 Q98Br4 P82096 Q93326 Q68p94 Q99193 Q9pr14 Q9pr14 Q9pr21 Q67838 Q67896 Q77896
Q7M1V1 Q9S8R4 E101 LITRU Q6SP94 Q99193 Q9PR14 Q9PR3 BRK ONCMY PNAS PRUDU URB3 MORMO Q67B52 BPP AGKHP
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6 6 6 6 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

ALIGNMENTS

RESULT 2
TWOF AEDAE

1D TMOP AEDAE

STANDARD; PRT; 10 AA.

C D1-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1990 (Rel. 45, Last annotation update)

DF 75-OCT-2004 (Rel. 45, Last annotation update)

DF TYPpsin-modulating oostatic factor (TMOF) (OOSH).

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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MEDIINE-22929740; PubMed-12890727; Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.; "Isolation and expression analysis of the canine insulin-like factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           MEDINE-92129337; PubMed=1733949;
MEDINE-92129337; PubMed=1733949;
Stracke M.L., Krutzach H.C., Unsworth E.J., Arestad A., Cioce V., Schiffmann E., Liotta L.A.

Schiffmann E., Liotta L.A.

"Identification, purification, and partial sequence analysis of autotaxin, a novel motility-stimulating protein.";

Discol. Chem. 267:2524-2529(1992).

NON TER 11 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Insulin-like factor 3 (Fragment).
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Last annotation update)
                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 26; DB 2; Li
100.0%; Pred. No. 2.3e+03;
Live 0; Mismatches 0;
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                                    11 AA.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
                                                                                          Created)
                                    PRT;
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                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, AUTOTAXIN (Fragment).
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                                                                                                                                                                                                               Homo sapiens (Human)
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MEDLINE=22643823; PubMed=12757776; DOI=10.1016/S0049-3848(03)00147-6; Hube F., Reverdiau P., Iochmann S., Cherpi-Antar C., Gruel Y.; Cheracterization and functional analysis of TFPI-2 gene promoter in a human choriocarcinoma cell line.";
                                                                                                                                                                           Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.; "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut."; FASEB J. 4:3015-3020(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and stops at 56 hrs.
PIR; A36454; A36454.
                                                                                                                                                                                                                                                                                                                                                STRAIN-Vero beach; TISSUR=Ovary;
MEDLINE=93357794; PubMed=835326; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=835326; DOI=10.1016/0965-1748(93)90044-S;
Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
"Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
Insect Biochem. Mol. Biol. 23:703-712(1993).
-! FUNCTION: Has an oostatic activity, Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBL_TaxID=7159;
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Pred. No. 2.1e+03;
0; Mismatches 2; Indels
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YD -> DY (in TMOF(B)).
236D0A7777776DC7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tissue factor pathway inhibitor-2 (Fragment).
Homo sapiens (Human).
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Pred. No. 1.5e+03;
0; Mismatches 1;
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                                                                                                                                                   MEDLINE=90367888; PubMed=2394318
                                                                                                                     STRAIN=Vero beach; TISSUE=Ovary;
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EMBL; AY044097; AAK72693.1; -.
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71.4%;
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80.0%;
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5; Conservative
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Class I integron DNA integrase (Fragment)

RESULT 4

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBI_TaxID=45631;
                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann
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GO; GO:0005739; C:mitochondrion; IEA
                                                                                                                         EMBL; AF173494; AAD51052.1; -.
GO; GO:0005739; C:mitochondrion; IEA
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4; Conservative
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Anas gracilis (Grey teal).
Mitochondrion.
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Best Local Similarity
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Best Local Similarity
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  Mitochondrion.
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                                                                                          MEDLINE-222709877; PubMed=12384388; Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin B., Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bradin C.; Lavenia A., Dolzani L.; Molecular characterization of integrons in epidemiologically unrelated clinical isolates of Acinetobacter baumannii from Italian hospitals reveals a limited Ddversity of gene cassette arrays."; Antimicrob Agents Chemother. 46:3665-3668(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Naturally occurring analogs of Lymantria testis ecdysiotropin, a gonadotropin isolated from brains of Lymantria dispar pupae."; Arch. Insect Biochem. Physiol. 36:37-50(1997).
-!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of larvae and pupae.
Direct protein sequencing.
SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIŠSUB=Brain;
MEDLINE=97387807; PubMed=9243792;
DOI=10.1002/(SICI)1520-6327(1997)36:1<37::AID-ARCH4>3.3.CO;2-3;
Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
                           Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Moraxellaceae, Acinetobacter.
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                                                                                                                                                                                                                                                  29.8%; Score 25; DB 2; Length 12; 62.5%; Pred. No. 3.6e+03; Live 0; Mismatches 3; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
ATPase 8 (Fragment).
Ansa castanea (Chestnut teal).
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Estis ecdysictropin peptide E (TE).
Lymantria dispar (Gypsy moth).
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Best Local Similarity 66.70,
Best Local 4; Conservative
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Best Local Similarity 62.55,
Conservative
             Acinetobacter baumannii.
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                                                                                 SEQUENCE FROM N.A.
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2 AIDPNP 7
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P80941;
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Q9TEN1
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
SEQUENCE FROM N.A.
Kennedy M., Spencer H.G.;
"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
Auk 117:154-163(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kennedy M., Spencer H.G.;
"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
Auk 117:154-163(2000).
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Archosauria, Aves, Neognathae, Anseriformes, Anatidae, Anas.
NCBI_TaxID=45630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 2; Length 14;
Pred. No. 4.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                         Score 25; DB 2; Length 14; Pred. No. 4.3e+03; 0; Mismatches 2; Indels
                                                                                                                         Mitochondrion.

NON_TER 1 1 SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.

NON_TER 1 1 SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
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Last annotation update)
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Query Match
Best Local Similarity 60.0-
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SEQUENCE FROM N.A.
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4 LDPSP 8
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PubMed=14762063; DOT=10.1101/gr.1329204;
Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
"Patterns of evolutionary constraints in intronic and intergenic DNA of Drosophila.";
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MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 2; Length 14;
Pred. No. 6.1e+03;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                            8 AA; 771 MW; C37775A771B5BDDA CRC64;
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EMBL; AY459549; AAR23007.1; -.
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Conservative
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076MKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UJL-2004 (TrEMBLrel. 27, Last annotation update)
15-UDL-2004 (TrEMBLrel. 27, Last annotation update)
15-UDL-2004 (TremBlrel. 27, Last annotation update)
16-UDL-2004 (TremBlrel. 27, Last annotation update)
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                                                                                                                                                                                                                                Length 10;
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Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ABO464871; BAB87160.11; GO; GO:0005739; C:mitochondrion; IEA. Mitochondrion.

NON TER 10

SEQÜENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
                                                                                                                                                                                                                                                                                        0; Indels
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                             Score 23; DB 2; I
Pred. No. 6.2e+03;
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Biochim. Biophys. Acta 1009:229-236(1989).
EMBL; Y18524; CAD5716-1; -
EMBL; X15424; CAA33464.1; -
GO; GO:0004872; F:receptor activity; IEA.
Lipoprotein; Receptor.
Lipoprotein; Receptor.
11 11 SEQUENCE 11 AA; 1221 MW; 373D041E272737
                                                                                                                                                                                                                                                                                     2; Mismatches
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MEDLINE=90089395; PubMed=2597675;
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=8804046; PubMed=3671079;

Musti A.M., Urshin, V.M., Avvedimento E.V., Zimarino V., Lauro R.D.;

Musti A.M., Urshin, V.M., Avvedimento E.V., Zimarino V., Lauro R.D.;

"A cell type specific factor recognizes the thyroglobulin promoter.";

Nucleic Acids Res. 15:8149-8166(1987).

BMBL; X06162; CAA29519.1;

PIR; 158273; 158273.

NON TER 12 12

12 1.41 MW; D7158AD39BD37732 CRC64;
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SEQUENCE FROM N.A.
MEDLINE=86235450; PubMed=3012778;
Habn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Habn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS.";
Science 232:1548-1553 (1986).
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Rat thyroglobulin gene (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NEBI_TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds cyclin II (By similarity).
SUBCELLULAR LOCATION: Nuclear; nucleolar.
MISCELLANEOUS: Isolates WM11, WM21, and WM31 were obtained from blood samples sequentially taken from a two-year old Haitian who was perinatally infected by her mother.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Transcriptional regulator that acts by binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAT protein (Transactivating regulatory protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 2; Length 12;
Pred. No. 7.5e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA; 1467 MW; 37CC737BFEF67AA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04610; LJFW.
HIV; M12507; TATSWMJA.
Activator; AIDS; Nuclear protein; RNA-binding;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last seq
05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12507; AAB12991.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 60.00,
10.00 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWVST 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAT_HV1W2
P12509;
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SEQUENCE
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TAT HV1W2
TAT HV1W2
TAT HV1W2
TO 01-OC
DT 01-OC
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27.4%; Score 23; DB 1; Length 14;

Query Match

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Best Local Similarity 80.0%; Pred. No. 8.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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8 8

Search completed: May 26, 2005, 19:40:36 Job time : 168 secs This Page Blank (uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

May 26, 2005, 19:22:57; Search time 159 Seconds (without alignments) 36.487 Million cell updates/sec

US-10-047-945-2 84 Title: Perfect score:

1 LKAMDPTPPLWIKTE 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

632537 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2003as:*geneseqp2003bs:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2004s:* geneseqp20028:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ption	75 N-termina	41 N-terminu				43 N-terminu	22 Synthetic			21 Human can	Human	54 Human can	43 Human can	75 Human can	21 Human can	48 Human can	06 Human can	94 Human can	38 Human can	25 Human can	83 Human can	16 Human can	27 Human can	63 Human can	52 Hydroxyme
Description	Aaw11575	Aaw53841	Abb80223	Abb80225	Abb80226	Aaw53843	Abb80222	Abb80227	Abb80228	Abr12621	Abr12017	Abr12854	Abr12743	Abr11875	Abr12121	Abr12948	Abr12106	Abr12294	Abr12738	Abr33125	Abr33383	Abr33116	Abr33427	Abr33363	Aaw21252
ΙD	AAW11575	AAW53841	ABB80223	ABB80225	ABB80226	AAW53843	ABB80222	ABB80227	ABB80228	ABR12621	ABR12017	ABR12854	ABR12743	ABR11875	ABR12121	ABR12948	ABR12106	ABR12294	ABR12738	ABR33125	ABR33383	ABR33116	ABR33427	ABR33363	AAW21252
DB	7	~	7	7	7	7	,	7	7	9	9	9	9	9	9	9	9	9	9	9	9	9	9	ø	~
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% Query Match	100.0	100.0	100.0	82.1	77.4	64.3	64.3	59.5	51.2	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	45.2
Score	84	84	84	69	65	54	54	20	43	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	38
Result No.	-	7	m	4	ιń	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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ABR11778 ABR12206 ABR12206 ABR12924 AAM39043 ABR12969 ABR12969 ABR12601 ABR12046 ABR12046 ABR12046 ABR12046 ABR12034 ABR12034 ABR12036 ABR12036 ABR12036 ABR12036 ABR12036	ADO72482 ADO64670 ADO65216
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	442 422.9 9.09.9
	36
22222222222222222222222222222222222222	4 4 4 6 4 6

ALIGNMENTS

Lethal toxin neutralising factor, LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite. N-terminal peptide from lethal toxin neutralising factor. AAW11575 standard; peptide; 15 AA. 94US-00310340. 93US-00058387. (revised)
(first entry) Didelphis virginiana. WPI; 1997-011287/01. Lipps FW, Lipps BV; (LIPP/) LIPPS B V. (LIPP/) LIPPS F W. 22-SEP-1994; 10-MAY-1993; 25-MAR-2003 20-MAR-1997 US5576297-A. 19-NOV-1996. AAW11575; AAW1157

Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal toxins - | peptide.

Claim 7; Col 9; 9pp; English.

The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-WAR-2003 to correct PF field.)

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(first entry)

Sequence 15 AA;

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                 ABB80223 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2002; 2002US-00047945.
                                                                                                                                          Synthetic LTNF, LT-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                      WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIPP/) LIPPS
(LIPP/) LIPPS
                                                                                                       06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                         24-JUL-2003.
                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                    ABB80223;
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RESULT 3
                  ABB80223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                   LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 84; DB 2; Length 15; 100.0%; Pred. No. 2.1e-06; ive 0; Mismatches 0; Indels
              Length 15;
                                                 Indels
              100.0%; Score 84; DB 2; I 100.0%; Pred. No. 2.1e-06;
                                                   0; Mismatches
                                                                                                                                                                                                              AAW53841 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00058387.
                                                                                                                                                                                                                                                                                                                                                                                                          histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00657163
                                                                                                         1 LKAMDPTPPLWIKTE 15
                                                                                  1 LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                     N-terminus of opossum LTNF,
                                                                                                                                                                                                                                                                                  (first entry)
            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Didelphis virginiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1993;
22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5744449-A.
                                                                                                                                                                                                                                                                                  08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1998.
                                                                                                                                                                                                                                               AAW53841;
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                                                                                                                                                                         RESULT 2
                                                                                                                                                                                            AAW53841
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ы Б. В.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine demainses (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, albertes, autoimmune disease (e.g. erythematosus (SLED), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, atthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzymen-linked immensoribent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins con be assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test, whereas an assay of proteins from the assayed by a simple ELISA test.
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                                                                                                  Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; *..
100.0%; *..
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 3; 24pp; English.
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Matches 15; Conservative
WPI; 2003-636703/60.
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RESULT 4 ABB80225

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1 LKAMDPTPPLWIKTE 15

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LKAMDPTPPLWIKTE

toxin neutralising factor; LTNF; serum protein; immunoglobulin E;

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IgE; nerve growth factor, NGF; insulin; myoglobin; adenosine deaminase; bbb; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an BLISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                              14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2002; 2002US-00047945
                                                              Synthetic LTNF, LT-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                             WO2003060471-A2
                                                                                                                                                                                                             saliva; ELISA
                     06-NOV-2003
                                                                                                                                                                                                                                                                                                                                    24-JUL-2003.
                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patient
                                                                                                     Lethal
  The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, c.g. Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva sample using an anti-serum that is specific for the protein. Saliva can be enertifuged immediately, whereas blood requires for serum. Saliva are centrifiquation to separate serum. Saliva proteins of the serum compared to blood collection as he served by a 
                                                                                                                                                              Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 7; Length 12;
Pred. No. 0.0004;
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100.0%; Pre
0; ?
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ABB80225 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-2002; 2002US-00047945
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                         Synthetic LTNF, LT-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                                                                        saliva; ELISA
                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-2003
                                                                                                                                                                                                                                                                                                                 Synthetic.
                                         ABB80225;
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e.g.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosinse deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invesive when compared to blood collection of perform Saliva can be centrifued immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW53843 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
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Gaps

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0; Indels

Mismatches

ABB80226 standard; peptide; 11 AA

ABB80226

ABB80226 ID ABB8 XX AC ABB8 RESULT 5

1 LKAMDPTPPLWI 12

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e.g.

US5744449-A. 28-APR-1998

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The sequences given in ABBB0222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & [1gB], nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and tracing conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva can learner learner that is specific for the protein. Saliva can be centrifuged immediately, whereas blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple BLISA test, whereas an assay of proteins from requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                              Assaying a human endogenous protein (e.g. 1gE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.078; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB80227 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 3; 24pp; English.
                                                                                                                              14-JAN-2003; 2003WO-US001044
                                                                                                                                                                            14-JAN-2002; 2002US-00047945
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                             Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-636703/60.
                                                                                                                                                                                                                               (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                          WO2003060471-A2.
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                                                                           24-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                           LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                              histamine reaction treatment
                                                                                                                                                                                                                                                                                                                                     96US-00657163
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N-terminus of opossum LINF
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1 LKAMDPTPPL 10
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                                                                                                                                                                            Didelphis virginiana
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Best Local Similarity
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Gaps

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WO2003060471-A2.

saliva; ELISA.

Synthetic.

saliva; ELISA

ABB80222;

RESULT 7

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Synthetic

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ABR1262:
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                                                                                                                                                                                                                          The sequences given in ABB80222-28 represent lethal toxin neutralising factor (INTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                            e.g.
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                                                                                                                                               Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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Pred. No. 1.8e+06;
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100.0%; Pred. No. 1...
'-- 0; Mismatches
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                                                                                                                                                                                                        Claim 7; Page 4; 24pp; English.
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                     14-JAN-2003; 2003WO-US001044.
                                           14-JAN-2002; 2002US-00047945
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Best Local Similarity 100.
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                                                                                                   Lipps BV, Lipps FW;
                                                                                                                         WPI; 2003-636703/60
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LIPPS F W.
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 24-JUL-2003
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gB), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva callection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 4; 24pp; English.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
14-JAN-2002; 2002US-00047945.
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                                                                                                                                                               Lipps BV, Lipps FW;
                                                                                                                                                                                                                      WPI; 2003-636703/60.
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Best Local Similarity
                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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6
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                                                                                                                                                                                                                                                                                                                                                                                            patient.
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Claim 13; Page 232; 1021pp; English.
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                       1 MDPSVPIWI
                                                                                                                                                                                                  from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200283921-A2.
                                                                                                                                                                                                                               Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR12854;
                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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                                                                                                                                                                            The present invention relates to novel human cancer-related genes and proteins (ABZ79120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                               New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
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   Hubert RS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; vaccine; cancer; immune response; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 6; Length 9;
Pred. No. 1.8e+06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer-related protein 156P1D4 HLA peptide #252.
   Ge W,
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Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Faris M,
                 Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morrison RK, Raitano AB;
                                                                                                                                                   Claim 13; Page 238; 1021pp; English.
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   PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                                                                                                             48.84;
 Challita-Eid
                                                                                                                                                                                                                                                                                                                                                                                                                         66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human leukocyte antigen.
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Best Local Similarity
Matches 6; Conserv
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1 MDPSVPIWI
                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
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Morrison K, N
   Jakobovits A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                 Morrison K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR12017;
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                                                                                                                                                                      diagnosis and/or progness of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                           proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The geneë and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the
present invention relates to novel human cancer-related genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer-related protein 156P1D4 HLA peptide #1089.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 6; I
Pred. No. 1.8e+06;
?; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jakobovits A, Challica-blu ...,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%;
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25-APR-2001; 2001US-0286630P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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ABR11875 standard; peptide; 10 AA.
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MDPSVPIWI
            MDPTPPLWI
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                                                                                                             ABR11875;
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                                                                                                                                                                              Human;
                                                                  RESULT 14
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            present
example
                                                                                                  Gaps
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as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The sequence is a human leukocyte antigen (HLA) peptide, used in an
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Pred. No. 9;
2; Mismatches 1; Indels
                                                                                                  1; Indels
                                                                            Length 9;
                                                                                                                                                                                                                                                                    Human cancer-related protein 156PlD4 HLA peptide #978.
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                                                                           Score 41; DB 6; L
Pred. No. 1.8e+06;
2; Mismatches 1;
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                                                                                                                                                                                                   ABR12743 standard; peptide; 10 AA.
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                                                                         48.8%;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                  Conservative
                                                                                                                        4 MDPTPPLWI 12
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MDPSVPIWI 9
                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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                                  from the invention
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                                                      Sequence 9 AA;
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                                                                                                                                                                                                                        ABR12743;
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ79168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humorral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                         cytostatic; vaccine; cancer; immune response; HLA;
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Human cancer-related protein 156P1D4 HLA peptide #110.
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jakobovits A, Challita-Eid PM, Faris
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 231; 1021pp; English.
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25-APR-2001; 2001US-0286630P.
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                                                                                         numan leukocyte antigen.
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MDPSVPIWI
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ID ABR1
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ABR12121;

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The present invention relates to novel human cancer-related genes and proteins (AB279120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humonral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                                                       Human, cytostatic, vaccine, cancer; immune response, HLA; human leukocyte antigen.
                                                                      Human cancer-related protein 156P1D4 HLA peptide #356.
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                                                                                                                                                                                                                                                                                                                                                                                                                Jakobovits A, Challita-Eid PM, Faris
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 233; 1021pp; English.
                                                                                                                                                                                                                                                                                                      10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
                                                                                                                                                                                                                                                                     10-APR-2002; 2002WO-US011654.
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-075555/07.
                                                                                                                                                                                                                                                                                                                                                                              (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                                                              WO200283921-A2.
                                                                                                                                                               Homo sapiens.
                                   19-MAY-2003
                                                                                                                                                                                                                                   24-OCT-2002.
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0; Gaps Score 41; DB 6; Length 10; Pred. No. 9; 1; Indels 2; Mismatches 48.8%; Query Match
Best. Local Similarity 66.7
Matches 6; Conservative

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4 MDPTPPLWI 12 |||: |:|| 1 MDPSVPIWI 9

ò 셤 Search completed: May 26, 2005, 19:37:43 Job time : 161 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

May 26, 2005, 19:40:44; Search time 134 Seconds (without alignments) 38.616 Million cell updates/sec

1 LKAMDPTPPLWIKTE 15 US-10-047-945-2 84 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

258160 Total number of hits satisfying chosen parameters: 1462099 segs, 344972447 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: / cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: / cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: / cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: / cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: / cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: / cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: / cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
14: / cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
15: / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: / cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
19: / cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
19: / cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
19: / cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 4, Appli	'n	Sequence 1, Appli	Sequence 6, Appli	Sequence 7, Appli	52	Sequence 444, App	Sequence 239, App	Sequence 735, App	Sequence 10923, A		Sequence 501, App
	ΩΙ	US-10-047-945-2	US-10-047-945-4	US-10-047-945-5	US-10-047-945-1	US-10-047-945-6	US-10-047-945-7	US-10-930-300-52	US-10-161-791-444	US-10-286-457-239	US-10-327-598-735	US-10-057-475B-10923	US-10-154-884B-10923	US-10-468-370-501
		14	14	14	14	14	14	17	14	14	16	15	15	15
	Query Match Length DB	15	12	11	10	0	&	6	15	12	12	σ	თ	13
οķο	Query Match	100.0	82.1	77.4	64.3	59.5	51.2	45.2	44.0	40.5	40.5	39.3	39.3	39.3
	Score	84	69	65	54	20	43	38	37	34	34	33	33	33
	Result No.	п	7	m	4	5	9	7	80	σ	10	11	12	13

502, 457,	Sequence 458, App	Sequence 252, App	52,	27,	~	ė	Sequence 70, Appl	16	16	188,	24,	198,	24,	Sequence 24, Appl	198,	192,	225,	•	225,	53,	168,	168,	480,	165,	165,	4, App	≥ 228€	Sequence 21, Appl	22,
US-10-468-370 US-10-468-496	16 US-10-468-496-458	38	15 US-10-116-275-52		14 US-10-254-905-27	9 US-09-845-583-13	US-1	0	US-1	US-1	-10-437	US-10-437			17 US-10-418-032-198	10 US-09-932-613-192	US-09-932	-09-932	10 US-09-932-322-225	-10	US-10	-10-418-032	US-10-190	15 US-10-437-708-165	US-10-41	9 US-09-995-804A-4	US-10	-10 - 437	15 US-10-437-708-22
13	13	12	12	13	13	14	14	14	14	0	13	13	13	13	13	14	14	14	14	15	۵	80	10	10	10	12	12	13	13
3 39.3 3 39.3	39.3	38.1	2 38.1	2 38.1	2 38.1	2 38.1	2 38.1	2 38.1	2 38.1	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	1 36.9	35.7					35.7	0 35.7	m	35.7
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ALIGNMENTS

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OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                Sequence 2, Application US/10047945

| Publication No. US2003015755A1
| Publication No. US2003015755A1
| GENERAL INFORMATION:
| APPLICANT: LIPPS, BINIE V. APPLICANT: LIPPS, BINIE V. APPLICANT: LIPPS, FREDERICK W. TITLE OF INVERTION: [195] IMPLICATED DISORDERS
| TITLE OF INVERTION: [195] IMPLICATED DISORDERS
| TITLE OF INVERTION: [195] IMPLICATED DISORDERS
| CURRENT APPLICATION UNMBER: US/10/047,945
| CURRENT FILING DATE: 2002-01-14
| PRIOR APPLICATION NUMBER: HOWER FILING DATE: NUMBER OF SEQ ID NOS: 7
| SOFTWARE: WORDERFECT 5.1 FOR WINDOWS |
| LENGTH: 15
| TYPE: PRY |
| ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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JS-10-047-945-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-047-945-2
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Publication No. US20030157555A1
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LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Corresponds to fragment 1-12 of 2 above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                       Sequence 4, Application US/10047945

Publication No. US2003015755A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

TITLE OF INVENTION: (19DIMPLICATED DISORDERS

TITLE OF INVENTION: (19DIMPLICATED DISORDERS

TILE REFERENCE: FWLAD15US

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: US/10/047,945

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5:1 FOR WINDOWS

SEQ ID NO 4

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10047945

Publication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (195) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATO15US

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT APPLICATION NUMBER: 2002-01-14

PRIOR APPLICATION NUMBER:

PRIOR PRICE OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 5

LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 14; Length 12; 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.1%; Score 69; DB 100.0%; Pred. No. 0.0:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10047945
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic.
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-047-945-5
                 US-10-047-945-4
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US-10-047-945-1
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LOCATION:
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NAME/KEY:
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APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILLING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
FILE REPERBANCE: FWLPATOLISUS
CURRENT APPLICATION NUMBER: US/10/047,945
FRIDR APPLICATION NUMBER: 0S/10/14/047,945
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE:
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Pred. No. 1.3e+06;
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100.0%; Pred. No....
0; Mismatches
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
OTHER INFORMATION: SYNTHESIZED.
OTHER INFORMATION: US 5,576,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic.
US-10-047-945-6
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.3
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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RESULT 9
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TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                             Corresponds to fragment 1-8 of 2 above.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, REEDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: GIPPILMEDIAN DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDFERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage COMPUTER: 18M PC COMPATIBLE COMPUTER: 18M PC COMPATIBLE OFFRATING SYSTEM: WINDOWS 95 SOFTWARE: MS WORD 6.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/930,300

FLILING DATE: 30-Aug-2004

CLASSIFICATION SANGE: 08/182,248

FLILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMMERION:
NAME: ALI KAMMERION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 14; L
Pred. No. 1.3e+06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 COlorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
SPOLGGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%; Scc...
100.0%; Pre
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/10930300 Publication No. US20050014138A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
; OTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match .
Best Local Similarity 100.
اتام 8; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                    APPLICANT: SPAKES, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 15;
                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
Score 38; DB 17;
Pred. No. 1.3e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/602,999
FILING DATE: 16 FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      US-10-161-791-444
; Sequence 444, Application US/10161791
; Publication No. US2030186863A1
; GENERAL INFORMATION:
; APPLICANT: SFARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Sequence 239, Application US/10286457 , Publication No. US20030166004A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (112) 669-9741/8864
TELEX: 66141 PENNIE
INPORMATION FOR SEQ 1D NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 790-9090
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Best Local Similarity 66.7
Matches 6; Conservative
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; MOLECULE TYPE: peptide
US-10-161-791-444
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                                                                                         5 DPTPPLW 11
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                                                                                                                                   1 DPTMPLW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
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APPLICANT: MCGRIAL, PATRICIA DIABNE APPLICANT: MCGRIALI, PATRICIA DIABNE APPLICANT: MCGRIALI, PATRICIA DIABNE APPLICANT: MCGRIALION COMPOSITIONS and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
FRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PELING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
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APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Marnion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,
TITLE OF INVENTION: Use Composition and Methods for the Detection, Diagnosis and Therapy,
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-0135210S
FILE REFERENCE: 014058-0135210S
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide US-10-057-475B-10923
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Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10923, Application US/10154884B
; Publication No. US20040005561A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.4
Pest Local Similarity 71.4
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|||| :|
3 PPLWNRT 9
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Publication No. US20040181039A1

GENERAL INFORMATION:

APPLICANT: Krah, Eugene

APPLICANT: Alyappa, Ashok

APPLICANT: Lawton, Canine Immunoglobulin Variable Domains, Caninized Antibodies, and

TITLE OF INVENTION: for Making and Using Them

TITLE OF INVENTION: for Making and Using Them

TITLE OF INVENTION: for Making and Using Them

TITLE OF INVENTION 10799-A

CURRENT APPLICATION NUMBER: US/10/327,598

CURRENT APPLICATION NUMBER: US 60/344,874

PRIOR PILLING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 1139

SOFTWARE: Patentin version 3.0

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based ; OTHER INFORMATION: ability to selectively bind to endothelial cells US-10-286-457-239
APPLICAMT: JENO GYURIS et al.
TITLE OF INVENTION: DENOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GFCI-P01-178
CURRENT FILING DATE: 2002-11-01
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/334822
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SSOFTWARE: Patentin version 3.1
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.5%; Score 34; DB 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 1.
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Publication No. US2004000206BA1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: canis familiaris; US-10-327-598-735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Aijun
Ordonez, Nadia
Carter, Lauren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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1 QSFDPTPP 8
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US-10-327-598-735
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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JS-10-468-370-502
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-154-8848-10923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 33; DB 15; Length 9; 71.4%; Pred. No. 1.3e+06; tive 1; Mismatches 1; Indels
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Publication No. US20040082039A1

GENERAL INFORMATION:
APPLICANT: Garr, Francis J.
APPLICANT: Garr, Francis J.
APPLICANT: Garter, Graham
APPLICANT: Garter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
APPLICANT: Waltiams, Stephen
APPLICANT: Watkins, John
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: MHC class II binding epitope US-10-468-370-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4
Matches 5; Conservative
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3 PPLWNRT 9
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US-10-468-370-501
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US-10-468-496-457
US-10-468-496
US-1
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                                                                                                                                                                                                                                   APPLICANT: Garry, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Garry, Francis J.
APPLICANT: Garry, Tim
APPLICANT: Garry, Garham
APPLICANT: Hamilton, Amitan
APPLICANT: Hamilton, Marian
APPLICANT: Hamilton, Marian
APPLICANT: Way, Joffrey
APPLICANT: Baker, Matthew
APPLICANT: Way, Joffrey
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: ARTIFICIAL PROFEINS WITH REDUCED
ITILE OF INVENTION: ARTIFICIAL
CURRENT FILING DATE: 2003-08-19
FRIOR FILING DATE: 2001-02-19
FRIOR PILING DATE: 2001-02-19
FRIOR PILING DATE: 2001-02-19
FRIOR PILING DATE: 2001-02-19
FRIOR PILING DATE: 2001-02-18
FRIOR PILING DATE: 2002-02-18
FRIOR FILING DATE: 2002-02-02-18
FRIOR FILING DATE: 2002-02-02-03
FRIOR FILING DATE: 2002-02-02-03
FRIO
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Sequence 502, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-03-15
APPLICATION WINBER: 01107012.5
APPLICATION NUMBER: 01106899.6
APPLICATION NUMBER: 01106899.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TPPLWIKT 14
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prior Filing Date: 2001-03-20

j. NUMBER OF SEQ ID NOS: 2036
j. SOFWARE: FastSEQ for Windows Version 4.0
j. SEQ ID NO 457
j. LENGTH: 13
j. TYPE: PRT
j. ORGANISM: Artificial Sequence
j. FEATURE:
j. OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-457
Query Match
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps
Oy
TPPLMIKT 14
Db
4 TSPTWIKT 11
Db
4 TSPTWIKT 11
Search completed: May 26, 2005, 19:53:55
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COUNTRY: USA
ZIP: 77401
                                                                                                                                                                                                                                                                                  US-08-310-340A-1
TELEX:
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Sequence 1, Appli
Sequence 2, Appli
Sequence 444, App
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Appli
Appli
Appl
                                                                       May 26, 2005, 19:32:43; Search time 43 Seconds (without alignments) 26.040 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-310-340A-1

US-08-67-163A-2

US-08-67-163A-2

US-08-602-999A-444

US-08-306-124-444

US-08-306-124-444

US-08-652-877-31

US-08-672-999A-252

US-08-672-999A-252

US-08-672-999A-252

US-09-268-992-70

US-09-268-992-70

US-09-547-691-10

US-09-547-691-10

US-09-327-446B-11

US-09-347-691-10

US-09-347-691-10

US-09-347-691-10

US-09-547-691-10

US-09-547-691-16

US-09-547-691-16
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US-09-995-804B-4
US-09-119-507B-21
US-09-119-507B-22
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                1 LKAMDPTPPLWIKTE 15
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                                                                                                                     US-10-047-945-2
84
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Match Length
                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 15
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                                                                              Run on:
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ORGANELLE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAR PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INFERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 1.OTH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 84; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                             TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINBAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
PRAGMENT TYPE: NO
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1 SOFTWARE: MS-WORD 0.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/657,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                            TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BINIE V. LIPPS STREET: 4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LKAMDPTPPLWIKTE 15
  SEQUENCE CHARACTERISTICS:
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOI
                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: 3-8 NOV 1991
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Patent No. 5744449

GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR

TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES: 3

CORRESPONDENCES: 3

CORRESPONDENCES: 3

CONFORT: BELLAIRE
STATE: TEXAS

COMPTRY: USA

STRET: 4509 MIMOSA DR.

STREET: 4509 MIMOSA DR.

COMPUTER: BELLAIRE
STATE: TEXAS

COMPUTER: BELLAIRE
STATE: TEXAS

COMPUTER: BELLAIRE

COMPUTER: BELLAIRE

SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION NUMBER: 08/310,340

FILING DATE: 12 SEPTEMBER 1994

CLASSIFICATION NUMBER: 08/058,387

FILING DATE: 10 NAMY 1993

ATTORING PATE: 10 NAMY 1993

ATTORING PATE: 10 NAMY 1993

ATTORING DATE: 10 NAMY 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 84; DB 1; Length 15; 100.0%; Pred. No. 1.2e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: IOTH WORLD CONCRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
                                             HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
NAMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLIBRAY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROGRAMME AND ABSTRACTS
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REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWI
FELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
INDIVIDUAL ISOLATE: TEXAS
DEVELOPMENTAL STAGE: ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
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Matches 15; Conservative
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TELEFAX: 713-663-7290
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-310-340A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES:
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Gaps

Gaps

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44.0%; Score 37; DB 3; Length 15; 66.7%; Pred. No. 19; 1; Indels tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FUBER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEMIT Release #1.0, Version #1.30
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION NUMBER: 08/602,999
FILING APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                    ; Sequence 444, Application US/09500124; Patent No. 6432920 GENERAL INFORMATION: GENERAL INFORMATION: Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 00.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
          15 amino acids
                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                            TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide
US-09-500-124-444
                                                                                                                                                                                                               2 KAMDPTPPL 10
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                             amino acid
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100.0%; Pred. No. 0.031;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REPRENCE/DOCKET NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
TELEPHONE: 713-663-7296
                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 444, Application US/08602999A Patent No. 6184205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THORN, Judith M.
QUILLIAM, Lawrence A.
DER, Channing J.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPARKS, Andrew B.
KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-602-999A-444
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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linear
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TOPOLOGY: li
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                 Sequence 31, Application US/08336343A
Patent No. 5677144
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Franke
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSES:
ADDRESSEB: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/08652877
Fatent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Crumley, Greeg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Morse, Clarence C.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 11;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-065
TELEPHONICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7.
                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: USA
ZIP: 19426-0107
US-08-336-343A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
TELEX: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ropology:
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APPLICANT: Akeretrom, Goran
APPLICANT: Akeretrom, Claes
APPLICANT: Rask, Lare
APPLICANT: Crunley, Gregg R.
APPLICANT: Moree, Clarence C.
APPLICANT: Morray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Thereof and DNA Encoding Same
CORRESPONDENCE: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 11;
80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Martin Savitzky
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
STREET: 3C43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB Pred. No. 80; 0; Mismatches
                                                                                                                                                   CLASSIFICATION: 435
PRIOR DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/487,314
PRIOR APPLICATION NUMBER: US 08/487,314
PRIOR DATE: 07-JUNE-1995
ATTORNEY/AGENT INPORMATION:
NAME: SAVILEXY, MARTÍN
FREFRENCE/ODCKET NUMBER: 29,699
REFERENCE/ODCKET NUMBER: 29,699
REFERENCE/ODCKET NUMBER: 3155E-US
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFRONE: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acide
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/08476515A Patent No. 6239270 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: PA

COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compag PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-652-877-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3C43,
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KPMPPRPPL 11
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MiSTOCK, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECPMUNICATION INFORMATION:
TELECPMUNICATION 1809-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-500-124-252

Sequence 252, Application US/09500124

Parent No. 6431990

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                           / MOLECTLE TYPE: peptide
US-08-602-999A-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-500-124-252
                                                                                                                                                                                                                                                                                                                                                                                                2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KPMPPRPPL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                       Matches
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Sequence 252, Application US/0860299A

Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: THORN, Judith M.

APPLICANT: THORN, Judith M.

APPLICANT: POWLKES, Dana M.

APPLICANT: POWLKES, Dana M.

TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPENDENCES: 467

APPLICANT: POMLES:

TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: New York

STREET: New York

STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1%; Score 32; DB 3; Length 11; 66.7%; Pred. No. 80; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN READABLE PATENTIN READABLE PATENTIN READABLE PATENTIN READABLE PATENTIN NUMBER: US/08/602,999A
                           PFILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
PILING DATE: 24-MAY-1993
ATTORNEY/AGRY INFORMATION:
NAME: SAVIEZKY, MARTÍN
NAME: SAVIEZKY, MARTÍN
PREGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELEPROMENICATION INFORMATION:
TELEPROMENICATION INFORMATION:
TELEPROMENICATION INFORMATION:
TELEPROME 610-454-3806
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
IENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO PERGIDE
HYPOTHETICAL: NO PERGIDE
HYPOTHETICAL: NO PERGIDE
HYPOTHETICAL: NO PERGIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPMPPRPPL 11
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Gaps
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APPLICANT: STATEM,
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: OUILIAM, Lawrence A.
APPLICANT: POWLKES, Dana M.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCES: 467
CORRESPONDENCE ADDRESS: Avenue of the Americas ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-ZIP:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
Score 32; DB 3; Length 12; Pred. No. 88;
                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
                                                                  0; Mismatches
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; ORGANISM: Homo sapiens
US-09-657-474-70
                                                                                                                                                                 7 TPPLW 11
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7 TPPIW 11
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                                                   Gaps
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APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
                                                                                                                                                                                                                                                   Sequence 70, Application US/09268992
Batent No. 6342351
GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
FILE REFERENCE: 7853-137
CURRENT APPLICATION NUMBER: US/09/268,992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Score 32; DB 4; Length 12;
Pred. No. 88;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION CHROMOSOMES: 121E REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/657,474
CURRENT APPLICATION NUMBER: US/09/657,474
CURRENT APPLICATION NUMBER: 09/266,992
PRIOR FILING DATE: 1999-03-16
PRIOR PELING DATE: 1999-01-22
PRIOR PELING DATE: 1999-01-22
PRIOR PLING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR PLING DATE: 1998-10-28
PRIOR PLING DATE: 1998-10-28
PRIOR PLING DATE: 1998-10-28
PRIOR PLING DATE: 1998-10-38
PRIOR PLING DATE: 1998-10-38
PRIOR PLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/078,044
PRIOR PLING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-03-16

EARLIER APPLICATION NUMBER: 09/236,134

EARLIER FILING DATE: 1999-01-22

EARLIER FILING DATE: 1999-01-28

EARLIER FILING DATE: 1998-10-28

EARLIER APPLICATION NUMBER: 60/088,312

EARLIER PILING DATE: 1998-06-05

EARLIER PILING DATE: 1998-06-05

EARLIER PILING DATE: 1998-06-05

SARLIER FILING DATE: 1998-06-05

SOFTWARE: FABELSQ for Windows Version 3.0

SEQ ID NO 70

LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09657474
Patent No. 6399762
    38.1%;
                                                 6; Conservative
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                                                                                                2 KAMDPIPPL 10
                                                                                                                                       4 KPMPPRPPL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
  Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 4; Conserv
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7 TPPIW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-657-474-70
                                                                                                                                                                                                                                   US-09-268-992-70
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LENGTH: 14
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GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 160
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (9)..(10)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (3)...(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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                  Length 14;
                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Burgeson, Robert
APPLICANT: Burgeson, Robert
APPLICANT: Champlaud, Marie-France
APPLICANT: Champlaud, Marie-France
APPLICANT: Hunter, Dale
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
FILE REPERENCE: 10287-056001
CURRENT APPLICATION NUMBER: US 60/200,863
PRIOR APPLICATION NUMBER: US 60/200,863
PRIOR APPLICATION NUMBER: US 60/200,863
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 13
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 4;
Pred. No. 1e+02;
1; Mismatches
                  Score 32; DB 3;
Pred. No. 1e+02;
                                                                Mismatches
                                                                                                                                                                                                                                             US-09-845-583A-13
; Sequence 13, Application US/09845583A
; Patent No. 6635616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-547-693-160
; Sequence 160, Application US/09547693
; Patent No. 6639050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.1%;
50.0%;
                  38.1%;
80.0%;
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ORGANISM: Artificial/Unknown
Query Match
Best Local Similarity 80.0
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Best Local Similarity 50.0
Matches 5; Conservative
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; ORGANISM: Mus musculus
US-09-845-583A-13
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US-09-232-446B-11

i Sequence 11, Application US/09232446B

j Sequence 11, Application US/09232446B

j Patent No. 6226647

j GENERAL INFORMATION:
    APPLICANT: VOYTES, Daniel F.
    APPLICANT: Gai, Xiaowu

    TITLE OF INVENTION: Integration to Specific Chromosomal Sites
    TITLE OF INVENTION: Integration to Specific Chromosomal Sites
    CURRENT APPLICATION NUMBER: US/09/232,446B

    CURRENT APPLICATION NUMBER: US 60/071,383
    PRIOR APPLICATION NUMBER: US 60/071,383
    PRIOR PILING DATE: 1998-01-15
    NUMBER OF SEQ ID NOS: 26
    SOFTWARE: PatentIN Ver. 2.0
    SEQ ID NO 11
                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: mxutant peptide; OTHER INFORMATION: sequence
US-09-232-446B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
; NAME/KEY: SITE

: LOCATION: (14)..(14)

; OTHER INFORMATION: The Proline at this position is a hydroxyproline.

US-09-547-693-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                          Query Match
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.9%; Score 31; DB 3; Length 13; Best Local Similarity 57.1%; Pred. No. 1.4e+02; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 26, 2005, 19:42:09 Job time: 44 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          3 AMDPTPPL 10
. :: |||||
4 SLTPTPPL 11
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4 SLDPSPP 10
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Tue May 31 05:58:01 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 19:51:16 ; Search time 38 Seconds (without alignments) 12.660 Million cell updates/sec

US-10-047-945-3 24 Title: Perfect score:

1 LKAMD 5 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

206 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
П	11	45.8	4	7	IS1049	metallothionein-A
7	11	45.8	2	7	A32516	cholecystokinin-5
ю	11	45.8	2	7	B31836	20K protein - Rick
4	σ	37.5	4	~	A48360	ŗ.
ហ	σ	37.5	4	~	PL0146	carbon-monoxide de
9	σ'n		4	7	JQ1273	neuropeptide Antho
7	σ	37.5	S	~	B41225	copper resistance
œ		37.5	ស	N	PT0624	
σ	σ	37.5	S	N	PT0651	T-cell receptor be
10	۵	33.3	S	~	855237	zinc-binding prote
11	7	. 29.2	m	ო	S13894	histidinol dehydro
12	7	29.5	4	~	A61300	22K superhelical D
13	7	29.5	4	~	140870	phospholipase C (E
14	7	29.5	4	N	T46627	hypothetical prote
15	7	29.5	4	~	E44823	synaptosomal-assoc
16	7	29.5	4	~	157745	D-mannonate hydrol
17	7	$\boldsymbol{\sigma}$	4	~	I40804	endoglucanase F -
18	9	25.0	e	٣	PT0578	T-cell receptor be
19	9	ഗ	4	~	S18401	thyroglobulin - do
20	9	25.0	4	~	A41890	protein D - Escher
21	9	25.0	4	N	S43014	hypothetical prote
22	9	25.0	4	N	D41654	hypothetical prote
23	9	25.0	4	~	B53284	cept
24	9	25.0	4	~	S47552	ubiquitin - rat
25	9	Ł.	4	~	A26209	protein-glutamine
56	9	25.0	4	~	140697	biotin A - Citroba
27	9	ഗ	4	N	A35779	neuropeptide Antho
28	ø	25.0	4	7	A32480	achatin-I - giant
59	9	25.0	4	7	PT0271	Ig heavy chain CRD

T-cell receptor be T-cell receptor be nentidyl-dimentida	, F G G	<pre>endo-1,4-beta-xyla angiotensin-conver photosystem I 10.4</pre>	neuropeptide - sea Ig heavy chain CRD Ig heavy chain CRD	Ig heavy chain CRD T-cell receptor be T-cell receptor be T-cell receptor be
PT0696 PT0711 JN0860	S70154 B60274 D60274	S70615 PQ0009 PQ0689	A60803 PT0267 PT0281	PT0308 PT0596 PT0513 PT0729
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30 31	9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	36 38 38	3 4 4 1 0 0 1	4 4 4 4 6 6 4 6

ALIGNMENTS

RESULT 1
IS1049
metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text change 21-Jul-2000
C; Accession: I51049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A; Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me.
A; Reference number: 151049; MUID:95324545; PMID:7601121
A;Accession: IS1049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A;Residues: 1-4 <ols></ols>
A; Cross-references: EMBL: X80181; NID: g1019799; PIDN: CAA56466.1; PID: g4379328
Oberv Match 45.8%: Score 11: DB 2: Length 4:
Similarity
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

~ S <u>B</u>-₽= 4 ઠે g

RESULT 2

Cholecystokinin-5 - dog
N.Alternate names: CCK-5
N.Alternate names: CCK-5
C.Species: Canis lupus familiaris (dog)
C.Species: Canis lupus
C.Species: Canis lupus
R.Spively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
A.; Spively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
A.; Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intess
A.; Reference number: A32516; MUID:87153871; PMID:3826354

A; Molecule type: protein
A; Residues: 1-5 <SH1>
C; Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystol C; Superfamily: gastrin
C; Superfamily: gastrin
C; Keywords: amidated carboxyl end; neuropeptide
F; 5/Modified site: amidated carboxyl end (Phe) #status experimental

0; Gaps Similarity 100.0%; Pred. No. 2.8e+05; 2; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 2; Conserv

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C;Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: JQ1273
R;Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.
R;Nothacker, H.P.; Rinehart, T.D.; Brimmelikhuijzen, C.J.P.
A;Title: Isolation of L.3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropep A;Reference number: JQ1273; MUID:92028852; PMID:1681803
A;Accession: JQ1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: The carboxyl-terminal amide probably arises from cleavage of a following glyc C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation F;I/Modified site: L-3-phenyllactic acid (Phe) #status experimental F;4/Modified site: amidated carboxyl end (Ala) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: B41225
R;Cha, J.S.; Cooksey, D.A.
R;Cha, J.S.; Cooksey, D.A.
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem A;Reference number: A41225; MUID:92020961; PMID:1924351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0624
R;Peeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
                                                                                                                                                                                                                                      C,Species: Anthopleura elegantissima
C,Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Experimental source: newborn thymus, strain BALB/c C, Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: P58705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translation not shown
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Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein A;Residues: 1-4 <NOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-5 < CHA>
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2 KA 3
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   ò
                     C;Species: Pseudomonas carboxydohydrogena
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-4-KRA>
A;Cross-references: UNIPROT:P19918
C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC 1.2.99.2) small chain - Pseudomonas carboxydohydrogena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cidence: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
Cidecession: A48360
Ficardy. D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.
Arch. Microbiol. 156, 477-483, 1991
A;Title: The methane monocxygenase gene cluster of Methylosinus trichosporium: cloning a freference number: A48360; MUD:92153031; PMID:1785954
A;Contents: OB3b
A;Accession: A48360
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 cCAR>
A;Residues: 1-4 cCAR>
A;Conse-reference: GB:S81887; NID:9245213; PIDN:AAB21391.1; PID:9245214
A;Note: sequence extracted from NCBI backbone (NCBIN:81887, NCBIP:81912)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subunit of Protein A - Methylosinus trichosporium (fragment)
C;Species: Methylosinus trichosporium
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carbo.
C;Species: Pseudomonas carboxydohydrogena
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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2.8e+05;
ches 0; Indels
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37.5%; Score 9;
Best Local Similarity 66.7%; Pred. No.
Matches 2; Conservative 1; Mismatc
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us-10-047-945-3.closed.rpr

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C;Species: Bscherichia coli
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61300
R;Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982
JyTitle: Purification and characterization of a protein from Escherichia coli which form
A;Reference number: A61300; MUID:83082696; PMID:6294066
A;Accession: A61300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000 C,Accession: 140870 R;Toyonaga, T.; Mateushita, O.; Katayama, S.; Minami, J.; Okabe, A. Mircobiol. Immunol. 36, 603-613, 1992 A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negati A;Reference number: 140870; MUID:92396045; PMID:1522810 A;Accession: 140870
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R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.

submitted to the EMBL Data Library, July 1995
A; Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 1-4 <KIS>
C,Comment: This protein resembles some of the histone-like protein of bacteria in amino
C,Keywords: DNA binding; monomer
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C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
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Amolecule type: DNA
A;Residues: 1-4 <RES.
A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417
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                                                                                             0; Indels
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Pred. No. 2.8e+05;
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                                          Score 7; DB 3; Lot
Pred. No. 2.8e+05;
1; Mismatches 0
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C; Keywords: dimer; NAD; oxidoreductase
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                                             29.2%;
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CiSpecies: Zea may8 (maize)
CiSpecies: Zea may8 (maize)
CiDate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
CiAccession: S55237
RiRobinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new family of zin A;Reference number: S55237; MUID:95234046; PMID:7717986
                                                                                                                                                                                                                                                                                                                                                                                                                                        beta chains have few N regions.
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histodinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
c;Species: Brassica oleracea (wild cabbage)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: $13894
R;Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: $13894; MUID:91112783; PMID:1989490
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                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PT0651
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
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                                                                    0; Indels
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A:Accession: PT0651
A:Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 cFEE.
A;Experimental source: day 4 postnatal thymus, strain BALB/C C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 9; DB 2; Length 5; 66.7%; Pred. No. 2.8e+05;
                 37.5%; Score 9; DB 2; Length 33.3%; Pred. No. 2.8e+05; ive 2; Mismatches 0; Ind
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A;Molecule type: protein
A;Residues: 1-3 «NAG»
A;Experimental source: var. capitata
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Matches 2; Conservative
                                                                    1; Conservative
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                 Query Match
Best Local Similarity
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RESULT 15
B44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N;Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: B44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Tille: The major 355-methionine-labeled rapidly transported protein (superprotein) is A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Reterns preliminary
A;Molecule type: protein
A;Residues: 1-4 < LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking
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29.2%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels
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A,Reference number: Z23105
A,Accession: T46627
A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Rolecule type: mRNA
A,Residues: 1-4 <-CHA>
A,Residues: 1-4 <-CHA>
A,Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A,Experimental source: strain s6PT2xs6PT3; 8 month seedlings
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29.2%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indele
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1 MK 2
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Search completed: May 26, 2005, 20:00:40 Job time : 40 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

May 26, 2005, 19:42:15; Search time 165 Seconds (without alignments) 15.518 Million cell updates/sec

US-10-047-945-3 24 LKAMD 5 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

23

seq length: 0 seq length: 5 四四四 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P19918 pseudomonas	P58705 anthopleura	Q08433 rattus sp.	P24272 vibrio fisc	P83568 sepia offic		_				P58707 anthopleura	P58648 octopus min							P38005 chlamydia t				P01162 macrocallis	P01858 homo sapien	homo		_	P82099 litoria rub	_	17 carcinus	P84182 eisenia foe
SUMMAKIES	TI	DCMS_PSECH	FFKA_ANTEL	Q08433	LUXE_VIBFI	ILME SEPOF	RE11_LITRU	P83073	ACH1_ACHFU		FLRF_HIRME	FLRN_ANTEL	OCP1_OCTMI	OCP3_OCTMI	Q160 <u>4</u> 7	BIOA_CITFR	FARP_CHICK	MPA4_JUNVI	TRM3_ECOLI	UXA4_CHLTR	GRWM_HUMAN	DCML_PSECH	FAR4_HIRME	FMRF_MACNI	TUFT HUMAN	Q96AT0	BIOB_CITFR	BPP7_BOTIN	EI03_LITRU	Q99007	AL14_CARMA	AP21_EISFO
4	match bength bb	4 1	4	4 2	3 1	4	5 1	5	4	4	4	4	4	4	4	5	5 1	5 1	5 1	5	3 1	4	4	4	4	4	5	5	5	5	2	2
% Query	March	37.5	37.5	37.5	σ	29.5	29.5	29.5	25.0		25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	16.7	16.7
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Result	. i	г	7	m	4	S	y	7	60	o	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	26		28	29	30	31

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Antho-Kamide.
Anthopleura elegantissima (Sea anemone).
Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;

P41853 artioposthi P67857 carcinus ma P67858 limilus pol P67859 periplaneta P67859 periplaneta P82071 litoria rub P82071 litoria rub P820731 homo sapien P8515 saccharomyc P8100 litoria rub P95615 saccharomyc P82100 litoria rub P58261 daucus carc P88261 daucus carc P88261 daucus carc
PARP ARTTR PRCT_CARMA PRCT_LIMPO PRCT_LITRU RE31_LITRU SUGA_ACHDO RE31_LITRU EOSI_HUMAN FYRI AWTEL YLMI YEAST E104_LITRU PSK DAUCA UC22_MAIZE UF01_MOUSE
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## ALIGNMENTS

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-1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
-1- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
-1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                            PIR; PL0146; PL0146.
2Pe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
Oxidoreductase.
                                                                                                                                                                                                                      Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                        Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                         4 4 AA; 420 MW; 6DD33DD6F000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 9; DB 1; Ler
llarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
              4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AA.
              PRT;
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              STANDARD;
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Best Local Similarity
                                                                                                                                                                 NCBI_TaxID=290;
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P58705;
              PSECH
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SEQUENCE
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DCMS_PSECH
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               X0008844446
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(Rel. 21, Created)
(Rel. 21, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                Vibrio fischeri.
                                                                                               NCBI_TaxID=668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LK 2
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P83568;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           MEDLINE-93391436; PubMed=8397415;
MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.,
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
-!-FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
                    MEDLINE=92028852; PubMed=1681803;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.,
Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a
novel neuropeptide from sea anomones ";
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Gunn;
MEDINNE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
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                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                    37.5%; Score 9; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                               PIR, J01273; J01273.
Amidation, Direct protein sequencing; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em. Biophys. Res. Commun. 177:1161-1164(1991).
$38636; AAB19259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 4 AA; 473 MW; 633732C42000000 CRC64;
                                                                                                                                                                                                                                      4 4 Alanine amide.
4 AA; 512 MW; 6DD339C9A0000000 CRC64;
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                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Local 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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ID LUXE VIBFI
AC P24272;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                            01-WAR-1992 (Rel. 21, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
TISSUE=Egg;
MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
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                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.2%; Score 7; DB 1; Length 3; 50.0%; Pred. No. 1.6e+06; ative 1; Mismatches 0; Indela
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"ILME: a waterborne pheromonal peptide released by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 3 AA; 374 MW; 6AA330300000000 CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Sepia officinalis (Common cuttlefish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M62812; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=9107226; PubMed=2254256;
                                                                               protein synthetase) (Fragment).
Name=luxE;
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Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to Swiss-Prot.
                                                                             Local Similarity
nes 1; Conserv
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ACH1_ACHFU
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Matches
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                                           The structure of new peptides from the Australin red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians,', Aust. J. Chem. 49:955-963 (1996).
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-i- MASS SPECTROMETRY: MW=598, METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
Amphibian defense peptide; Direct protein sequencing.
SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
      Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk sperm-
attracting peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1396;
                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                       29.2%; Score 7; DB 1; Length 4; 50.0%; Pred. No. 1.6e+06;
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Last annotation update)
                                                                                                     Direct protein sequencing; Pheromone. SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;
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                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Rubellidin 1.1.
                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, AND MASS SPECTROMETRY.
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                                                                                                                                                                1; Conservative
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Best Local Similarity
1; Conserve
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3 MB 4
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REIL LITRU
AC PRILL LITRU
AC PRES-2003
DT 28-FEB-2003
DT 28-FEB-2003
DT 05-JUL-2004
DE Rubellidin 1
OS Litoria rube
OC Amphibia; Ba
OC Amphibia; Ba
OC Amphibia; Ba
OC Pelodryadina
OX NCBI TaxID-1
RN [1]
RN [1]
RN [1]
RA SEGUBNCE, AN
RA STEINDORNER
RA STEINDORNER
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RA STEINDORNER
RA STEINDORNER
RA TYPLE M.J.
RT TYPLE M.J.
RT TYPLE M.J.
RT TANGELLUO
RT OF GEVOLUTION
CC -1- FUNCTION
CC -1- MASS SPE
KW Amphibian G SEQUENCE G
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01-OCT-2003
                                                                                                                                        Query Match
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                                                                                                                                                              Matches
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-I- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata n., Iwashita T., Nomoto K.; Iwashita T., Nomoto K., Nomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Sigmurethra, Achatinoidea, Achatinidae, Achatina.
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                                                                                                                                                                                                                                                     Gaps
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Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
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                                                                                                                                                                                                                                               0; Indels
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                                                                                                             29.2%; Score 7; DB 2; Length 5; 50.0%; Pred. No. 1.6e+06; tive 1; Mismatches 0; Indele
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5 AA; 623 MW; 6B01AAA336F00000 CRC64;
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4 AA; 408 MW; 6AADD9C810000000 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achatina fulica (Giant African snail).
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MEDLINE-91264856; PubMed-1675568;
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MEDLINE=89273551; PubMed=2597281;
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Conservative 0
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                                                                                                         STANDARD;
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Matches 1: Conser
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Antho-RNamide,
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<u>::</u>:
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                                                                                                         FLRN ANTEL
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                                                                                      FLRN ANTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                               MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
                                                                                                                                                                                                                                              Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L., Identification of RFamide neuropeptides in the medicinal leech.", Peptides 12:897-908(1991).
- SUBCELLULAR LOCATION: Secreted.
- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
                                                                                 FMRFamide-like neuropeptide YLRF-amide.
FMRFamide-like neuropeptide YLRF-amide.
Hundo medicinalise (Medicinal leech).
Bukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helisoma trivolvis (Snail).

Eukaryota, Metazoa, Annelida, Clitellata, Hirudinida, Hirudinea, Arhynchobdellida, Hirudiniformes, Hirudinidae, Hirudo.

NCBI_TaxID=6421, 27815,
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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
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Pred. No. 1.6e+06;
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MOD_RES 4 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
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MOD RES 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
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                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                  4 AA.
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                  PRT;
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                  STANDARD;
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Matches 1; Conserval
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Best Local Similarity
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                HIRME
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P42561;
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FLRF_HIRME
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--- SUBCELLIULAR LOCATION: Secreted.
--- PTTM: Ocp-2 has L-Phe instead of D-Phe.
--- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
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"Cardioactive peptides isolated from the brain of a Japanese octopus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
-!- TASS SPECIFORTRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
--- PIR, A35779; A35779.
--- Amidation; Direct protein sequencing; Neuropeptide.
--- MOD_RES 1 1 3-phenyllactic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=90319122; PubMed=1973541;
Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
Reinscheid R.K., Nothacker H.-P., Staley A.L.;
"Isolation of L.3-phenyllactyl-Leu-Arg-Ann-NH2 (Antho-RNamide), a sanemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                  Bukaryota; Merazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
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Peptides 2::633-630(2000).
-!-FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less:
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MOD RES 2 2 D-phenylalanine (in form Ocp-1)
SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.0%; Score 6; DB 1; Length 4; 50.0%; Pred. No. 1.6e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 4 Asparagine amide.
4 AA; 549 MW; 64540729A0000000 CRC64;
                                                                                                                                                   (Rel. 41, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Cardioactive peptides Ocp-1/Ocp-2.
4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AA
                                                                                                                                                                                                                                                                                                       Anthopleura elegantissima (Sea anemone)
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Search completed: May 26, 2005, 19:59:10
                                  InterPro; IPR001806; Ras_trnsfrmng.
PRINTS; PR00449; RASTRNSFRMNG.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwakoshi E., Hisada M., Minakata H.; "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.3; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
D-amino acid; Direct protein sequencing; Hormone.
MOD_RES 2 D-serine (in form Ocp-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Cardioactive, has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92062171; PubMed=1840490;
MercKen L., Moras V., Hemon L., Litonne B., Bousseau A.,
Dautry-Varsat A., Collins M., Mayaux J.F.;
"An exon 5-deleted mRNA encodes a functional interleukin 2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Octopus minor (octopus).
Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005525; F:GTP binding; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0007264; P:small GTPase mediated signal transduction; IEA.
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                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                               Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 6; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 2 D-serine (in form Ocp-4).
4 AA; 463 MW; 6AB365BB10000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
EMBL: 864248; AAB20279.1; -.
HSSP: P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                           DB 1; Len
5. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
25.0%; Scc...
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides 21:623-630(2000).
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                 Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=89766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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AC 28-FEB-2003
DT 28-FEB-2003
DT 28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia col:
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBL_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                           ..
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PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Adenosylmethionine-8-amino-7-oxonomancate aminotransferase
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                             Query Match 25.0%; Score 6; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 1; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Score 6; DB 1; Length 5; Similarity 100.0%; Pred. No. 1.6e+06; 1; Conservative 0; Mismatches 0; Indele
4 AA; 525 MW; 69CAB769A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase.
NON_TER 5 5
SEQUENCE 5 AA; 582 MW; 6AAABIBIA6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 A.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: Pyridoxal phosphate
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aminotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Job time : 168 secs

OM protein - protein search, using sw model

May 26, 2005, 19:41:29 ; Search time 157 Seconds (without alignments) 12.317 Million cell updates/sec Run on:

US-10-047-945-3 24

1 LKAMD S Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

45841 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 5 8 8 8 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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No.	Score	Match	Length	BB	ΩI	Description	
7	24	100.0	ស	7	AAW53842	Aaw53842 N-terminu	: 2
0	24	100.0	S	7	ABB80224	Abb80224 Synthetic	Ų
٣	21	87.5	ß	~	AAW24922	Aaw24922 Vesicular	H
4	16	66.7	4	7	ABR82923	Abr82923 Tetrapept	ň
S	16	66.7	S	Ŋ	AAM49579	Aam49579 Human bet	ñ
9	15	62.5	2	ო	AAY83346	Aay83346 Peptide	E
7	15	62.5	5	4	AAM51285	-	_
80	15	62.5	2	4	AAB35188	Aab35188 Human T	Tra
σ	15	62.5	S	7	ADJ82602	Adj82602 Shuffled	_
10	15	62.5	5	7	ADJ82644	Adj82644 Shuffled	_
11	15	62.5	ß	œ	ADM46700	Adm46700 C-termina	ផ
12	15	62.5	2	æ	ADM46839	Adm46839 Variant	æ
13	15	62.5	2	80	ADM46841	Adm46841 Variant	ಹ
14	15	62.5	2	8	ADQ95007	Adq95007 Synthetic	Ö
15	14	58.3	4	7	AAR83230	_	
16	14	58.3	4	7	AAY08030	Aay08030 Biotin de	ē
17	14	58.3	4	m	AAY88365	Aay88365 CCR inhib	ą
18	14	58.3	4	ß	AAU74705	Aau74705 Human cel	ď
19	14	58.3	2	7	AAR91816	Aar91816 Mab-425-C	ب
20	14	58.3	5	4	AAM51340	Aam51340 Anti-HIV	_
21	14	58.3	S	'n	ABB46284	Abb46284 Desmoglei	٦,
22	14	58.3	2	Ŋ	AA015010	0 Mutant	ΗM
23	14	58.3	5	7	ADF53341	Adf53341 Adeno-ass	8
24	13	54.2	4	(7)	AAW08855	Aaw08855 Peptide	υ
25	13	54.2	4	7	AAW48196	Aaw48196 Conantoki	::::

Aaw49978 Conantoki Aay67411 Caspase p Aay67211 Caspase p Aab29561 Human cas Aag79033 Amino aci Aag79037 Peptide w Aam50477 Peptide w Aam50477 Peptide w Aam50477 Antiflamm Abg7672 Antiflamm Abg76418 Antiflamm Adj4613 Apoptosis Adv67576 Amino aci Aar5983 Peptide a Aax5983 Peptide m	Adusassa repunde #Adil0462 Cell surf Abg75419 BIVM N-te
AAW49978 AAY2412 AAY2412 AAY267511 AAB29561 AAB30774 AAB30774 AAB30774 AAB30774 AAB30774 AAB30774 AAB4013 AAB76148 ADV762852 ADV76583	AAU85930 AD110462 ABG75419
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 10 10 10 11 (10 10 14 4 4 4 10 10 10 10 10 10 10 10 10 10 10 10 10	0 <b>10 10</b>
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22222222222222222	111
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# ALIGNMENTS

AAW53842

AAW53842 standard; peptide; 5 AA.

AAW53842;

(first entry) 08-JUL-1998

N-terminus of opossum LTNF.

LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment. 

Didelphis virginiana.

USS744449-A.

28-APR-1998

96US-00657163. 03-JUN-1996; 93US-00058387. 94US-00310340. 10-MAY-1993;

22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV;

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

Claim 5; Col 13; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemozrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

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LKAMD
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                                  Sequence 5 AA;
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31-JAN-1991;
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17-OCT-1997
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                                                                                            Query Match
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Matches
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snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; ElE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; ealiva; ELISA.
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                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                100.0%; Score 24; DB 2; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB80224 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2003; 2003WO-US001044.
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                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic LTNF, LT-5
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                                                                    to horse proteins
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                                                                                                                                  Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods to determine the etiological agent of autoimmune diseases such as systemic lupus erythematosus (SLB). A common antigen for SLB and closely related disorders is the 60 kD protein-RNA particle: Ro/SSA, present in all cells studied to date. Staphylococcus VB protease digestion of this protein reveals bands of 51, 40, 35, 28 and 13 kD which are strongy immunoreactive with SLB autoantibodies. From the 13 kD band, peptide AAW24911 demonstrated maximal antigenicity against anti-Ro/SSA autoantibodies peptides immunoreactive with SLB autoantibodies can then be used to screen for other peptides reactive with the antibodies. An example of such a peptide is the sequence presented here which is derived from the nucleocapsid protein of the Indiana serotype of the vesicular stomatitis virus. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Etiological agent; autoimmune disease; systemic lupus erythematosus; SLB; Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
                                                                       Gaps
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      Length 5;
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                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vesicular stomatitis virus nucleocapsid protein #2.
100.0%; Score 24; DB 7; I
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                   AAW24922 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vesicular stomatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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                                                                    Conservative
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                              Local Similarity
nes 5; Conserv
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RESULT 5

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The invention relates to increasing or reducing cell apoptosis. The method involves providing at least 1 cell or a tissue, and a polypeptide having 1 or more defined tetrapeptide sequences selected from ARR8293-28 and administering the polypeptide to the cell so that apoptosis of the cell or tissues is increased or reduced. The polypeptide is selected from a human, mouse or a rat CCAAT/enhancer binding protein (C/Babbeta). The cell or tissues is increased or reduced. The polypeptide is selected from the compositions are useful for diagnoshing (C/Babbeta). The certing cancer, fibrosis or cell apoptosis in a tissue. The fibrosis is confered with rejection, alcoholism, toxic liver disease, genetic hepaticis binfection, alcoholism, toxic liver disease, genetic converted with a liver cirrhosis. The cell apoptosis is a secciated with a liver disease from rejection of liver converting converting associated with a liver disease from rejection of liver converting converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, hepatic disease, brain damage, neurological trauma, neurodegeneration, myocardial infarction, arteriosclerosis, fibrotic skin conditions and fibrotic pulmonary disease. The present sequence represents a tetrapeptide obtained from exemplary mouse and human c/EBPbeta polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or
                                                                                                                                                                                                                                                                            C/BBPbeta; apoptosis; CCAAT/enhancer binding protein; hepatotropic; virucide; vulnerary; vasotropic; nephrotropic; ophthalmological; cytostatic; cerebroprotective; neuroprotective; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing or reducing cell apoptosis, for diagnosing, preventing and treating cancer, fibrosis, ischemia, Alzheimer's disease, myocardial infarction and arteriosclerosis, comprising using novel tetrapeptide
                                                                                                                                                                                                                        Tetrapeptide sequence derived from C/EBPbeta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                   cardiant; nootropic; human; mouse
                                                      ABR82923 standard; peptide; 4 AA.
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buck M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-721701/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2003
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                                                                                                             ABR82923;
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RESULT 4
                               ABR82923
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This invention describes novel peptides (1) of the defensin type which have antibacterial, antiinfertility and contraceptive activity and which can be used for peptide therapy. (1), and their derivatives and can be used for peptide therapy. (1), and their derivatives and cassociated will respiratory or urogenital tracts, or of the skin and associated algands; (11) to treat systemic diseases associated with overexpression or deficiency of defensin production, particularly as ubstitution therapy or by using (1)-specific antibodies; (ii) to treat infertility, sepecially where the result of disordered sperm penetration, infartion or maturation, also as contraceptives; and (iv) as a diagnostic marker of inflammatory disease in epithelial organs. Both chronic and coute diseases may be treated, e.g. in intensive care. Also genes that canced (1) can be used for systemic or localised gene therapy of the specified diseases, in epithelial tissues or organs. (1) have exceptional conventional describty well suited for long-term use. This sequence represents a human defensin described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New defensin type peptides useful for treatment of bacterial infections and for fertility control, and as a diagnostic marker of inflammatory disease in epithelial organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                          Defensin; human; antibacterial; antiinfertility; contraceptive; peptide therapy; infection; gastrointestinal; respiratory tract; urogenital tract; skin; gland; sperm penetration; systemic disease; infertility; sperm inidation; sperm maturation; diagnostic marker; inflammatory disease; epithelial organ; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.8e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 16; DB 5; Length 5; 60.0%; Pred. No. 1.8e+06;
                                                                                                                          Human beta-defensin hBD-7 peptide fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adermann K;
                  AAM49579 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY83346 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 22; 41pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conejo-Garcia J,
                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2001; 2001WO-EP007973.
                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2000; 2000DE-01033505.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IPFP-) IPF PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-179697/23.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           WO200204487-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5 AA;
                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forssmann W,
                                                                                        28-MAY-2002
                                                                                                                                                                                                                                                                                                                                               17-JAN-2002
                                                    AAM49579;
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ID AAY8
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AAM49579
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0; Gaps

66.7%; Score 16; DB 7; Length 4; 75.0%; Pred. No. 1.8e+06; ive 1; Mismatches 0; Indels

Local Similarity 75.0 nes 3; Conservative

Matches

Query Match

KAMD 5

8 8

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The invention relates to peptides (AAMS1251-AAMS1381) with a higher affinity to gp120, part of the outer shell of HIV, than known peptides. CC affinity to gp120, shown by formula (H-) H-)A2-A3-A4-A5-R. C(1), A1-A2-A3-A4-A5-R. (2) or H-A1-A2-A3-A4-A5-R. (3), (H-) a1-a2-a3-a4-5-R. (2), A1-A2-A3-A4-A5-R. (2), A1-A2-A3-A4-A5-R. (3), (H-) a1-a2-a3-a4-A5-R. (2), A1-A1, G1V, A81 or Tyr residue; A2 = Va1, A8p, Trp, L9s, Phe, CC L9s, Va1, G1V, G1Y, A81 or Tyr residue; A3 = L9s, Va1, A8p, Arg, Phe, Trp, Pro or Tyr residue; R = OH derived CC Asn, G1N, His, Lys, Arg, Phe, Trp, Pro or Tyr residue; R = OH derived CC Asn, G1N, His, Lys, Arg, Phe, Trp, Pro or Tyr residue, R = OH derived C Lys, Va1, G1V, G1V, A8n or Tyr residue, or a polypeptide residue having optional amino acids at N-terminal; A5' = G1Y, A1, G1V, A1, L9, L1C, Trp, Pro or Tyr residue, or a polypeptide residue having optional amino acids at C-terminal; a1 = Tyr, CC Thr, Met, Asn, G1N, His, Dys, Arg, Phe, Trp, Pro or Tyr residue; a2 = Arg Tyr, Try, Trp, Has or Arg, Phe, G1Y, Trp, His or Arg, Phe, G1Y, Trp, His or Arg, Phe, G1Y, Trp, His or Arg, Phe, Tyr, Arg, G1N, His, Lys, Arg, Phe, G1Y, A1, Va1, Leu, His, Ser, Thr, Met, Asn, G1N, His, CL, Ser, Thr, Met, Asn, G1N, His, CC Try residue, or a polypeptide residue having optional amino acids at C-terminal; and a5' = G1Y, A1a, Va1, Leu, His, Ser, Thr, Met, Asn, G1N, His, CC Terminal; and a5' = G1Y, A1a, Va1, Leu, His, Ser, Thr, Met, Asn, G1N, CH, Leu, His, Lys, Arg, Phe, Tyr or Try, or Try, or Olypeptide residue having optional amino acids at C-terminal; and a5' = G1Y, A1a, Va1, Leu, His, Ser, Thr, Met, Asn, G1N, CH, Leu, His, Lys, Arg, Phe, And, Phe, Tyr or Try, or Try, or Try, or Dolypeptide residue having optional amino acids at C-terminal. The peptides are useful in the treatment of HIV and in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; protein degradation; siah-mediated degradation protein; SMDP; SFC-complex protein; SCP; siah-latlpha; siah-latine protein; SCP; Skpl-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division; Skpl-associated destruction-box protein; inflammatory disease.
                                                                                                                                                                                                             Novel peptides with affinity to gp 120, useful for treatment of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 4; Length 5; Pred. No. 1.8e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Traf 6 aptamer clone peptide SEQ ID NO: 39.
                                                                                                                                                                                                                                                                 Example 2; Page 8; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35188 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
75.0%;
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11-JAN-2000; 2000JP-0006182.
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                                                      11-JAN-2000; 2000JP-00006182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                       WPI; 2001-605354/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200077207-A2
                                                                                                         (FUJI/) FUJII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VKAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences encoding SDD1, a subtilisin-like serine protease, can be used to produce transgenic plants with altered stomata characterisitics. These plants exhibit improved freshness, increased dry weight, reduced leaf temperatures, reduced water loss and lower water consumption and for enhancing the sugar and/or protein content of plant leaves, modulating photosynthesis under high intensity conditions or for the improvement of disease resistance of plants. The transgenic plants and cells of such plants are useful in the preparation of feed, food or additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant DNA molecules encoding subtilisin-like serine protease, useful for producing transgenic plants with altered stomata, lower water consumption and enhanced diseased resistance.
                                                                                                                                                       SDD1; serine protease; subtilisin; transgenic plants; dry weight; stomata; sugar; water; protein; CO_2; H_2O; CO2; H2O; crop protection; feed; foodstuffs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%; Score 15; DB 3; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-HIV; vaccine; gp120; human immunodeficiency virus.
                                                                                                    Peptide motif of SDD1 subtilisin-like serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-HIV peptide with affinitiy to gp120 number 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM51285 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-EP007633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98EP-00119244
                                                   (first entry)
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                                                                                                                                                                                                                                                           Synthetic.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berger D, Altmann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317995/27.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1998;
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                                                   16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000
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  AAY83346;
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RESULT 7 AAM51285

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Synthetic.
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                                                                                                                                           The present invention provides the protein and coding sequences of several siah-mediated degradation proteins and SCF-complex proteins. These are designated Siah-Lalpha, Siah-1 interacting protein (SIP), which encodes two proteins clark to alternative splicing (SIP-L and SIP-S), Skplassociated F-box protein-lalpha and beta and -2 (SAF-Lalpha, SAF-lbeta and SAF-2) and Skpl-associated destruction-box protein (SAD). The proteins and their coding sequences are useful in the diagnosis and treatment of cancers, disorders where too little cell division occurs such as bone marrow aplassas, immunodeficiencies and inflammatory diseases including sepsis, fibrosis, arthritis and graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
                                                                            Siah-Mediated Degradation Protein, useful for drug screening, for therapeutic applications and for functional genomics.
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                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                        Length 5;
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Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                             62.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                    Example 15; Page 71; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ82602 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BECT ) BECTON DICKINSON & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-2002; 2002WO-US031165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-2001; 2001US-0333476P.
                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.00
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shuffled KLMSY peptide #13.
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                          Matsuzawa S;
(BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dean C, Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAAL/) HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-505179/47.
                                                  WPI; 2001-071273/08
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                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ82602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
                         Reed JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
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The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contexted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Glu-Glu-Glu-Glu-March-Ser-Tyr. (P3) Phe-Phe-Phe-Pro-Val (P5). Lys-Lys (P4) Phe-Phe-Phe-Phe-Phe-Cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders. myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a shuffled P3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; meuroblastcoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
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                                                                                                                                                                                                                                                                                                                                                                         . 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                    Length 5;
                                                                                                                                                                                                                                                                                                                                                                    DB 7;
                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 7
Pred. No. 1.8e-1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 425; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ82644 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spargo CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BECT ) BECTON DICKINSON & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-2002; 2002WO-US031165.
                                                                                                                                                                                                                                                                                                                                                                62.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2001; 2001US-0333476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shuffled KLMSY peptide #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dean C, Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAAL/) HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-505179/47.
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                                                                                                                                                                                                                                                                                                                          Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
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C-terminal of CDRH3

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variant; CDRH3; CDR; complementarity determining region; antibody;
                                                                                                                                               Variant antibody variable domain peptide,
                                                                   ADM46839 standard; peptide; 5 AA.
                                                                                                                                                                                       domain; phage; library; antigen
                                                                                                                                                                                                                                                                                             03-JUN-2003; 2003WO-US017545.
                                                                                                                                                                                                                                                                                                                       03-JUN-2002; 2002US-0385338P
                                                                                                                                                                                                                                                                                                                                    16-APR-2003; 2003US-0463656P
                                                                                                                       03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                          WO2003102157-A2
    AMD
                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                    11-DEC-2003.
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                                                                                             ADM46839;
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                                                      ADM46839
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Lys-Lys (P4) Phe-Phe-His-Pro-val (P5) . (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a shuffled P3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide useful for selecting antigen for antigen binding variable domain that binds to target antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel polypeptide comprising a variant CDRH3 antibody variable domain. The invention further provides an antibody phage library. The variant CDRH3 polypeptide is useful for selecting an antigen for an antigen binding variable domain that binds to a target. The phage library is useful for selecting a polypeptide that binds to a target target antigen from the library of polypeptides and isolating high affinity binders to a target antigen from the library of polypeptides and isolating high expression vectors. This sequence represents a variable antibody domain related polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  variant; CDRH3; CDR; complementarity determining region; antibody;
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                                                                                                                                   Score 15; DB 7; Length 5;
Pred. No. 1.88+06;
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.larity 100.0%; Pred. No. 1.8e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 4; 205pp; English.
                                                                                                                                                                                                                                                                                             ADM46700 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 domain; phage; library; antigen
                                                                                                                                               62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2002; 2002US-0385338P.
16-APR-2003; 2003US-0463656P.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                         C-terminal CDRH3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sidhu SS;
                                                                                                                                                                                                                   1 LKSM 4
                                                                                                                                                                                                   1 LKAM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003102157-A2
                                                                                                                       Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                 03-JUN-2004
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                                                                                                       polypeptide useful for selecting antigen for antigen binding variable
                                                                                                                                                                                                                              The invention relates to a novel polypeptide comprising a variant CDRH3 antibody variable domain. The invention further provides an antibody phage library. The variant CDRH3 polypeptide is useful for selecting an antigen for an antigen binding variable domain that binds to a traget. The phage library is useful for selecting a polypeptide that binds to a target antigen from the library of polypeptides and isolating high affinity binders to a target antigen from the library of polypeptides and isolating high expression vectors. This sequence represents a variable antibody domain related polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variant; CDRH3; CDR; complementarity determining region; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variant antibody variable domain, CDRH3 C-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 15; DB 8; Le
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                     Disclosure; SEQ ID NO 163; 205pp; English.
                                                                                                                                  domain that binds to target antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM46841 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; phage; library; antigen.
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                                                    WPI; 2004-043102/04.
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Best Local Similarity
Matches 3; Conserv
Sidhu SS;
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This invention relates to a novel polypeptide comprising a variant complementarity determining region of heavy chain 3 (CDRH3) region complementarity determining region of heavy chain 3 (CDRH3) region comprising at least one structural amino acid position, and at least one structural position having a variant amino acid. The invention is constructural position having a variant amino acid. The invention is cast cast density as aconte for identifying novel antigen binding polypeptides are useful as source for identifying novel antigen binding polypeptides and antibody cast can be used therapeutically or as reagents. A synthetic antibody phage library of these polypeptides is useful for screening synthetic antibody or antigen binding polypeptide with a streening synthetic antibody or antigen binding polypeptide with the library is also useful as resource for identifying immunoglobulin polypeptide sequences that are capable of interacting with any of a wide variety of target molecules. The invention provides high throughput, efficient and automatable systems for screening antigen binding molecules of interest. The present sequence is that of a peptide which is related to the novel polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cysteine contg. peptide derivs. which inhibit platelet integrin - are useful for treating or preventing circulatory disease, thrombosis, etc., also for affinity purification. of integrins.
                                 New polypeptide comprising variant complementarity determining region of heavy chain 3 having structural amino acid positions, and non-structural positions having variant amino acid, useful for identifying antigen binding polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  platelet integrin; gp IIb/IIIa; thrombosis; infarction; inflammation; coronary heart disease; arteriosclerosis; atherosclerosis; stroke; angina pectoris; tumour; osteoporosis; angiogenesis; restenosis; awound healing; ligand; integrin; affinity chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 15; DB 8; Length 5; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
                                                                                                                   Disclosure, SEQ ID NO 4; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Integrin-inhibiting peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felding-Habermann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR83230 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93DE-04336758.
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Best Local Similarity
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 WPI; 2004-580713/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                    New polypeptide useful for selecting antigen for antigen binding variable domain that binds to target antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region; heavy chain 3; CDRH3; CDRH3 scaffold; synthetic antibody phage library; binding affinity; structural stability;
                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel polypeptide comprising a variant CDRH3 antibody variable domain. The invention further provides an antibody phage library. The variant CDRH3 polypeptide is useful for selecting an antigen for an antigen binding variable domain that binds to a target. The phage library is useful for selecting a polypeptide that binds to a target antigen from the library of polypeptides and isolating high affinity binders to a target antigen from the library of polypeptides and isolating high expression vectors. This sequence represents a variable antibody domain related polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic phage antibody library-related 4D5 antibody peptide SeqID4.
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                                                                                                                                                                                                                                                                                                                       Disclosure; Page 7; 205pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ95007 standard; peptide; 5 AA.
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18-JUL-2003; 2003US-0488610P.
08-OCT-2003; 2003US-0510314P.
                                                                                  03-JUN-2003; 2003WO-US017545.
                                                                                                                03-JUN-2002; 2002US-0385338P.
16-APR-2003; 2003US-0463656P.
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Best Local Similarity 100...
3; Conservative
                                                                                                                                                                  (GETH ) GENENTECH INC
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               WO2003102157-A2
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Unidentified.
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                                                 11-DEC-2003
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The invention relates to new linear peptides of formula X-A-Cys(R1)-B-Z in which X is H or Ac; A is absent or is Asp or a specified polypeptide; B is absent or a specified amino acid or polypeptide; A and B cannot both be absent; and Z is OH or an ester or amide group. The peptides inhibit binding of the platelet integrin gpIIb/IIIa to its natural ligands and so are useful for preventing circulatory diseases, thrombosis, cardiac infarction, inflammation, coronary heart disease, arteriosclerosis, atherosclerosis, stroke, angina pectoris, tumour, osteoporosis, angiogenesis and restenosis. They are also useful for promoting healing of wounds and as ligands for purification of integrins by affinity chromatography. The present sequence is a specific example of the *888888888888888888

Sequence 4 AA;

ö Gaps ö Query Match 58.3%; Score 14; DB 2; Length 4; Best Local Similarity 75.0%; Pred. No. 1.8e+06; Matches 3; Conservative 0; Mismatches 1; Indels

2 KAMD 5

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1 KAAD 4

Search completed: May 26, 2005, 19:56:21 Job time : 165 secs

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May 26, 2005, 19:59:17 ; Search time 134 Seconds (without alignments) 12.872 Million cell updates/sec
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1: \cgn2 \( \) \cgn2 \( \) \cgn \( \)
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1462099 segs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                              OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					COLUMNICO	
Result		& Query				
No.	Score	Match	Match Length DB ID	8	QI.	Description
7	24	100.0	S	14	US-10-047-945-3	Sequence 3, Appli
8	15	62.5	5	16	US-10-679-246-39	Sequence 39, Appl
m	15	62.5	2	17	US-10-783-311-107	Sequence 107, App
4	15	62.5	ហ	17	US-10-759-731A-4	Sequence 4, Appli
S	14	58.3	4	σ	US-09-016-750C-17	Sequence 17, Appl
9	14	58.3	4	0	US-09-016-869B-17	Sequence 17, Appl
7	14	58.3	4	10	US-09-947-206-17	Sequence 17, Appl
ω	14	58.3	Ŋ	σ	US-09-817-661-26	Sequence 26, Appl
6	14	58.3	S	14	US-10-099-442-2	Sequence 2, Appli
10	14	58.3	5	17	US-10-911-065-2	Sequence 2, Appli
11	13	54.2	4	13	US-10-115-704-9	Sequence 9, Appli
12	13	54.2	4	14	US-10-357-467-33	Sequence 33, Appl
13	13	54.2	4	17	US-10-808-187-88	Sequence 88, Appl

Sequence 93, Appl Sequence 110, Appl Sequence 110, Appl Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 110, Appl Sequence 110, Appl Sequence 20, Appli Sequence 20, Appli Sequence 12, Appl Sequence 14, Appl Sequence 14, Appl Sequence 20, Appl Sequence 15, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 131, Appl Sequence 22, Appl Sequence 21, Appl Sequence 22, Appl Sequence 134, Appl Sequence 134, Appl Sequence 134, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl	467, 115, 22, A
5 15 US-10-156-214A-93 4 9 US-09-015-10 4 9 US-09-915-306-5 4 9 US-09-915-306-6 4 9 US-09-915-306-7 4 9 US-09-915-306-7 4 9 US-09-915-306-8 4 9 US-09-915-306-8 4 9 US-09-915-374-6 4 9 US-09-915-374-6 4 14 US-10-915-374-8 4 15 US-10-915-374-8 4 16 US-10-915-374-8 5 US-09-915-374-8 6 US-09-915-374-8 7 US-09-915-374-8 8 US-09-915-374-8 9 US-09-915-374-8 16 US-10-806-018-110 5 9 US-09-915-374-20 5 10 US-09-915-374-20 5 10 US-09-915-374-20 5 11 US-10-006-869-3019 6 US-10-395-032-3019 7 US-10-395-032-3019 8 US-10-395-032-3019 9 US-10-395-032-3019	17 US-10-808-187 17 US-10-938-249 17 US-10-773-032
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## ALIGNMENTS

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                                                                                                                                                                                                                           APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: (195) IMPLICATED DISORDERS
TITLE OF INVENTION: (195) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT APLICATION NUMBER:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 3
LENGTH: 5
LENGTH: 5
TYPE: PRIOR PLILIS OF SEQUENCE
CONTACTH: 5
CON
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Sequence 3, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: SYNTHESIZED.; OTHER INFORMATION: US 5,576,297. US-10-047-945-3
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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,750C
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1997
PRIOR APPLICATION NUMBER: US 08/306,511
PRIOR APPLICATION NUMBER: US 08/306,511
PRIOR DATE: 14-SEP-1994
PRIOR DATE: 14-SEP-1994
PRIOR DATE: 12-SEP-1994
PRIOR DATE: 12-SEP-1994
PRIOR DATE: 25-MAY-1994
PRIOR DATE: 25-MAY-1994
PRIOR DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 15; DB 17; I
100.0%; Pred. No. 1.3e+06;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: C-terminal of CDRH3 of 4D5 US-10-759-731A-4
PRIOR APPLICATION NUMBER: US 60/441,059
PRIOR FILING DATE: 2003-01-16
PRIOR PLILOR DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/510,314
PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATION NUMBER: US 07/963,308
DATE: 16-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/227,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09016750C
Patent No. US20020025305A1
                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.5
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 14-APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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STREET: CAL.
THY: BOSTON
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US-09-016-750C-17
                                                                                                                                                                                             SEQ ID NO 4
                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                LENGTH:
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                               Sequence 39, Application US/10679246

Publication No. US20040163138A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Mateuzawa, Shu-ichi

TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto

TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto

TITLE OF INVENTION: UN Protein Degradation, Products and Methods Related Thereto

CURRENT APPLICATION NUMBER: US/10/679,246

CURRENT FILING DATE: 2003-10-02

PRIOR APPLICATION NUMBER: US 90/591,694

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 50

SEQ ID NOS: 50

LENGTH: 5

LENGTH: 5
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APPLICANT: Bond, Christoper J.
TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
FILE REFERENCE: 11669.136USUJ
CURRENT APPLICATION NUMBER: US/10/759,731A
CURRENT FILING DATE: 2004-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetically generated peptide US-10-783-311-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 62.5%; Score 15; DB 16; L Similarity 100.0%; Pred. No. 1.3e+06; 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQUENCE 107, Application US/10783311
FUBLICATION NO. US20050009136A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: PAPP-A LIGANDS
TILLE OF INVENTION: PAPP-A LIGANDS
TILLE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
CURRENT FILING DATE: 2004-02-19
PRIOR PILING DATE: 2004-02-19
PRIOR FILING DATE: 2003-02-19
NUMBER OF EXQ ID NOS: 394
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.5%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 3; Conservative 0; Mismatches
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Publication No. US20050079574A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapien
US-10-679-246-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
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US-10-759-731A-4
                          US-10-679-246-39
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APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Serrano, Manuel.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Ropes & Gray
STREET: One International Place
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.3%; Score 14; DB 9; 18est Local Similarity 75.0%; Pred. No. 1.3e+06; Matches 3; Conservative 0; Mismatches 1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: VAICENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.13
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordead
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/016,869B
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/26,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,912
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/27,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
FILING DATE: 18-NOV-1993
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09016869B Patent No. US20020082392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide US-09-016-750C-17
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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USA
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COUNTRY:
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Gaps
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US-09-17, Application US/09947206

Sequence 17, Application US/09947206

Publication No US20030100489A1

GENERAL INFORMATION:

Beach, David H.

Serrano, Manuel

Serrano, Manuel

TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES

RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,206
FILING DATE: 04-Sep-2001
FILING DATE: 19-80-01-03
APPLICATION NUMBER: 09/016,750
FILING DATE: 1998-01-03
APPLICATION NUMBER: US 08/306,511
FILING DATE: 1998-01-03
APPLICATION NUMBER: US 08/20,511
FILING DATE: 18-8EP-1994
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APPL-1994
APPLICATION NUMBER: US 08/227,371
FILING DATE: 11-APPL-1994
APPLICATION NUMBER: US 08/227,371
                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
                                                                                                                                                                                                                                                                                                                                                                                     58.3%; Score 14; DB 9; I
75.0%; Pred. No. 1.3e+06;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matchew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-DEC-1992
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18-0CT-1993
ATTORNEY/AGENT INPORMATION:
NAME: Vincent, Matthew P.
REGISTRATION INMERS: 36,709
REFERENCE/DOCKET NUMBER: 36,719
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7739
TELEPAN: (617) 951-7050
INFORMATION FOR SEQ ID No: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/154,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 07/991,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.v.
3; Conservative
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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Gaps

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Joseph Control of Squence 2, Application US/10911065

j Edguence 2, Application US/10911065

j Publication No. US20050069927A1

GENERAL INFORMATION:

APPLICANT: Lockhart, David J.

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

FILE REFERENCE: 3016.28

CURRENT APPLICATION NUMBER: US/10/911,065

CURRENT FILING DATE: 2004-08-04

PRIOR PILING DATE: 2002-03-14

PRIOR FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Version 3.1

LEVICHART FILING DATE: 1909-05-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Version 3.1
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                                                                                                                                                                                                      ö
                                                                                                                                                      58.3%; Score 14; DB 14; Length 5; 100.0%; Pred. No. 1.3e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Publication No. US20020192780A1

GENERAL INFORMATION:
APPLICANT: SCHW, JOON HONG
TITLE OF INVENTION: NOVEL ANTI-INFLAMMATORY, PEPTIDES
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/115,704

CURRENT PILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: KR10-2001-21598

PRIOR APPLICATION NUMBER: 11

NUMBER OF SEQ 1D NOS: 11

SOFTWARE: Kopatent In 1.71

FEASTOLD 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%; Score 14; DB 17;
100.0%; Pred. No. 1.3e+06
:ive 0; Mismatches C
                                                                                , OTHER INFORMATION: Synthetic sequence. US-10-099-442-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INPORMATION: SYNTHETIC
                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                  2 KAM 4
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US-10-115-704-9
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LENGTH: 5
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                                                                     FEATURE:
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US-10-099-442-2
Sequence 2, Application US/10099442
Fublication No. US20030129604A1
GENERAL INFORMATION:
APPLICANT: Lockhart, David J.
APPLICANT: Wong, Gordon G.
TITLE OF INVENTION: Identification of Molecular Sequence Signatures and Methods Invol:
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
CURRENT APPLICATION UNDER: US/10/099,442
CURRENT PILING DATE: 2002-03-14
FRIOR PILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Mutagenized; CTHER INFORMATION: sequence
US-09-817-661-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Osbourn, Jane
APPLICANT: Holet, Thor
TITLE OF INVENTION: Improvements to ribosome display
FILE REFERENCE: 84633
                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/817,661
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/193,802
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09817661
Patent No. US20020076692A1
                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                           TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                 LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Gaps

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Sequence 93, Application US/10156214A

Publication No. US20040001801A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edwin L. Madison
APPLICANT: George P. Vlasuk
APPLICANT: George P. Vlasuk
APPLICANT: Scort Jeffrey Kemp
APPLICANT: Mallareddy Komandla
APPLICANT: Daniel Vanna Siev
APPLICANT: Daniel Vanna Siev
APPLICANT: TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic Us
TITLE OF INVENTION: Thereof
FILE REFERENCE: 24745-1611
CURRENT PILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.2%; Score 13; DB 17; I 100.0%; Pred. No. 1.3e+06; tive 0; Mismatches 0;
                                                            Sequence 88, Application US/10808187
Publication No. US200500090091
GENERAL INFORMATION:
APPLICANT: PETRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 3; Conserva
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                                                                                      Gaps
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                                             Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEB: Rothwell, Figg, Ernst & Manbeck, p.c.
STREET: 1425 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4;
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llarity 100.0%; Pred. No. 1.3e+06;
Conservative 0; Mismatches 0;
                                         54.2%; Score 13; DB 13;
50.0%; Pred. No. 1.3e+06;
ive 1; Mismatches 1;
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2314-256.A
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                        Cruz, Lourdes J.
Olivera, Baldomero M.
Walker, Craig
Colledge, Clark
Hillyard, David R.
Jimenez, Elsie
TITLE OF INVENTION: Conantokins
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                        Sequence 33, Application US/10357467
Publication No. US2030194729A1
GENERAL INFORMATION:
APPLICANT: Abogadie, Fe C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                      Query Match
Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserva
                                                                                                                           2 KAMD 5
                                                                                                                                                     1 KVLD 4
                                                                                                                                                                                                                               RESULT 12
US-10-357-467-33
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US-10-115-704-9
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Publication No. US20040002102A1
| Publication No. US20040002102A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Litman, Gary W. US20040002102A1| A. APPLICANT: Litman, Gary W. US20040002102A1| A. APPLICANT: Hawke, No. US20040002102A1| A. APPLICANT: Hawke, No. US20040002102A1| A. APPLICANT: Hason, Donna D. TITLE OF INVENTION: Transcriptional Products, and Uses Thereof FILE REFERENCE: US-103X
| TITLE OF INVENTION: Transcriptional Products, and Uses Thereof CURRENT FILING DATE: 2003-04-16
| NUMBER OF SEQ ID NOS: 64
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 59
| LENGTH: 5
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                                                                                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                                                                     0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0;
                                                  FEATURE:

CATION: 1

COCATION: 1

COCATION: 1

FEATURE:

NAME/KEY: MOD_RES

COTHER INFORMATION: Alanine-therapeutic agent
US-10-156-214A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 26, 2005, 20:12:33
Job time : 172 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (3)...(3)
COTHER INFORMATION: Xaa = Val or Cys
US-10-417-476-59
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                  FEATURE:
OTHER INFORMATION: Conjugate
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Best Local Similarity 50.0°
Matches 2; Conservative
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2 KXLD 5
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2 LKA 4
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US-10-417-476-59
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TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 3
HYPOTHETICAL: YES
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77401
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Sequence 413, Appl
Sequence 413, Appl
Sequence 39, Appl
Sequence 88, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 33, Appli
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                                                                                                                                           May 26, 2005, 19:50:26; Search time 40 Seconds (without alignments) 9.331 Million cell updates/sec
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Sequence 55,
Sequence 40,
Sequence 14,
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Sequence 3
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lssued Patents AA:*
1: /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-335-198-20

US-08-319-20

US-09-104-337A-413

US-09-591-694-39

US-08-329-820-4

US-08-329-820-4

US-08-34-147B-17

US-08-346-147B-17

US-08-947-214D-17

US-08-947-214D-17

US-08-581-918A-17

US-08-333-219B-2

US-08-585-21028

US-08-933-219B-2

US-08-933-219B-3

US-08-933-818-33

US-09-142-078-33

US-09-142-080-33
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S-09-142-078-33
S-09-351-141-33
S-09-142-080-33
S-09-142-080-33
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PCT-US93-12679-40
US-08-208-108-14
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                                                                                                                                                                                                                                                                                                                                                                                                                   513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           US-10-047-945-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                            1 LKAMD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 5
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                                                                                                                                                Run on:
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No.
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Sequence 7, Appli
Sequence 8, Appli
Sequence 160, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       NGS-08-657-163A-3

Sequence 3, Application US/08657163A

Fatent No. 574440.

GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: SYNTHETIC LIPRES AND THEIR

TITLE OF INVENTION: SYNTHETIC LIPRES AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES:

ADDRESSEE: BINIE V. LIPPS

STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STRATE: TEXAS

COUNTRY: USA
                           US-09-162-366C-9
US-09-162-366C-8
US-09-162-366C-8
US-09-915-374-6
US-09-915-374-6
US-09-915-374-6
US-09-915-374-7
US-09-915-374-7
US-09-915-306-5
US-09-915-306-6
US-09-915-306-6
US-09-915-306-6
US-09-915-306-8
US-09-915-366-2
US-09-915-366-39
US-09-18-366C-30
US-09-18-366C-30
US-09-187-8859-437
US-09-187-8859-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OCMPUTER: 1BM COMPATIBLE
OCMPUTER: 1BM COMPATIBLE
OCMPARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION 1514
PRIOR APPLICATION NUMBER: 08/310,340
FILING DATE: 10 MAY 1993
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 28,387
FILING DATE: 10 MAY 1993
ATTORNEY AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: FWL. PAT-US-011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 713-482-29 TELEFAX: 713-663-7290
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          Patent No. 5962255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-350-260A-413
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| Sequence 20, Application US/08335198 |
| Patent No. 5637454 |
| TITLE OF INVENTION: Diseases |
| TITLE OF INVENTION PACHATES |
| TITLE OF INVENTION DATA: Google |
| TITLE OF INVENTION DATA: DISEASES |
| TITLE OF INVENTION DATA: 
                                                                                                            Length 5;
                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 4.1e+05;
                                                                                                      100.0%; Score 24; DB 1; I 100.0%; Pred. No. 4.1e+05;
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                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-JAN-1991
ATTONNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMF 114CIP
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: (404)815-6508
TELECOMUNICATION SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-350-260A-413
; Sequence 413, Application US/08350260A
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          SYNTHETIC
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                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Best Local Similarity
Matches 4; Conserv
; ORIGINAL SOURCE:
US-08-657-163A-3
                                                                                                                                                                                                                                          1 LKAMD 5
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APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT PILING DATE: 200-06-09
EARLIER PILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 39
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: PELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIPPARNN, FELDERICH

ITILE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC Compatible

OPERATING STERMEN: PC Compatible

OPERATING STERMEN: DE 4000 Wersion #1.30 (BPO)

CUNFRENT APPLICATION NUMBER: US/08/329,820

FILING DATE: 28-OCT-1994

JCLASSIFTATION: S30

PRIOR APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

SECTEMATION NUMBER: MERCK 1635

TELECOMMUNICATION INFORMATION:

NAME: HAMLEL-KING, DIANA

TELECOMMUNICATION NUMBER: MERCK 1635

TELECOMMUNICATION NUMBER: MERCK 1635

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 15; DB 4; Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-243-6410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-591-694-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                      Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION OF SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PETENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
PRIOR DATE: 25-Jun-1998
PRIOR APPLICATION NUMBER: US 08/350,260
PRILICATION NUMBER: US 08/350,260
PRILICATION NUMBER: US 08/350,260
APPLICATION NUMBER: GB 9110549,4
PRILING DATE: 15-MAY-1991
APPLICATION NUMBER: PCT/GB92/00883
PILING DATE: 24-MAR-1992
APPLICATION NUMBER: US 08/150,002
PRILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
PRILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
PILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
PILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
PILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 4; Length 5; Pred. No. 4.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 413:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 413: US-09-104-337A-413
                          Sequence 413, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Materhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.v
-Log 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KAMD 5
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US-09-104-337A-413
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Gaps

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0; Indels

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                                Length 4;
                                                     i; Indels
                               Score 14; DB 1;
Pred. No. 4.1e+05;
0; Mismatches 1
                                58.3%;
N-terminal
                                                      3; Conservative
                               Query Match
Best Local Similarity
Matches 3; Conserv
         US-08-329-820-4
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; Sequence 39, Application US/09591694

US-09-591-694-39 RESULT 5

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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTER READABLE FORM:

COUNTER READABLE FORM:

COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: WAS PLOYDY disk
COMPUTER: WAS PLOYDY disk
COMPUTER: WAS PLOYDY DATA:
SOFTWARE: WAS PLOYDY DATA:
APPLICATION NUMBER: US/08/581,918A
TILING DATE: 30-UM-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-UM-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APP-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-APR-1994
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTONEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
REFERENCE/DOCKET NUMBER: MATCHEW P.
REGISTRATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-346-147B-17
Sequence 17, Application US/08346147B
Patent No. 6211334
GENERAL INFORMATION:
APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
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Matches 3; Conserv
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-581-918A-17
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                                                                                                                                                                                                                                                                                                                Sequence 88, Application US/08329820
; Sequence 88, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
APPLICANT: FILDING-HABERMANN, BRUNHILDE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER: INPR PC compatible
COMPUTER: INPR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: MERCK 1635
TELECOMMUNICATION NUMBER: MARCK 1635
TELERAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 88:
SEGUENCE CHARACTERISTICS:
LENGTH: 4 amin on acide
SEGUENCE CHARACTERISTICS:
LENGTH: 4 amin on acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; Score 14; DB 1; Length 4; 75.0%; Pred. No. 4.18+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product= "Lys(BOC)"
OTHER INFORMATION: /note= "N-terminal: FMOC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 4
; OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-581-918A-17
; Sequence 17, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KAAD 4
                                                                                                                         2 KAMD 5
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                                                                                                                                                                                   1 KAAD 4
                                                                                                                                                                                                                                                                                                       US-08-329-820-88
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Gaps
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Sequence 17, Application US/09016750C

Patent No. 6486131

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Demetrick, Douglas J.

APPLICANT: Hannon, Manuel

APPLICANT: Hannon, Gregory J.

TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES

TITLE OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%; Score 14; DB 3; 75.0%; Pred. No. 4.1e+05tive 0; Mismatches
                                                                                               SIREDIA OUE FOR CILLUE CHARLE CITY: Boston CITY: Boston COUNTY: USA ZIP: 0.2109

COUNTY: USA ZIP: 0.2209

COMPUTER READABLE FORM: MEDIUW TYPE: FLOSPY disk COMPUTER: WardPad CURRENT APPLICATION DATA: PC-DOS/MS-DOS SOFFWARE: WardPad CURRENT APPLICATION NUMBER: US/08/497,214D FILING DATE: 30-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/346,147

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/248,812

FILING DATE: 14-SEP-1994

PRIOR APPLICATION NUMBER: US 08/248,812

FILING DATE: 14-SEP-1994

PRIOR APPLICATION NUMBER: US 08/27,371

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/227,371

PRIOR APPLICATION NUMBER: US 08/154,915

FILING DATE: 18-NOV-193

PRIOR APPLICATION NUMBER: US 08/154,915

FILING DATE: 17-DEC-1993

PRIOR APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1993

ATTORNEY APPLICATION DATA: APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.05
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
          NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-08-497-214D-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                            ADDALL
STREET: CALL
TWY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KARD 4
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APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08497214D
Patent No. 6331390
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%; Score 14; DB 3; Length 4; 75.0%; Pred. No. 4.1e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
COMPUTER: READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOORDED
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APP-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 07/991,997
FILING DATE: 110-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                         CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KAMD 5
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APPLICANT: Lockhart et al.
APPLICANT: Lockhart et al.
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Identification of Molecular Sequence
TITLE OF INVENTION: Signatures and Methods Involving the Same
FILE REFERENCE: 3016.11
CURRENT APPLICATION NUMBER: US/08/933,219B
CURRENT FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/025,740
PRIOR FILING DATE: 1996-09-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM disk
COMPUTER: PROCRAPHIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,523
FILING DATE: 06-NOV-1992
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 94114572.4
FILING DATE: 16-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISORATION NUMBER: Merck 1717
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESTAX: 703-243-6410
TELEEX: 64191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 14; DB 2; Length 5;
    NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
; OTHER INFORMATION: Synthetic Sequence US-08-933-219B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-933-219B-2; Sequence 2, Application US/08933219B; Patent No. 6329140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 64191
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                  CITY: Arlington
                                                                                                                      STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KAM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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LENGTH: 5
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Pred. No. 4.1e+05;
                                                                                 CUNTAR: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATENIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,750C
FILING DATE: 30-JAN-1998
RIDR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-ARR-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 17-DEC-1992
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1993
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18-OCT-1993
ATTOMERY/AGENT INFORMATION:
APPLICATION NUMBER: PCT/US93/09945
FILING DATE: 18-OCT-1993
ATTOMERY/AGENT INFORMATION:
APPRICATION NUMBER: 26.709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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REPERBNICK/OCKET NUMBER: MIV-071.13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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Patent No. 5824782
GENERAL INFORMATION:
APPLICANT: Hoelzer, Wolfgang
APPLICANT: von Hoegen, Ilka
APPLICANT: Strittmatter, Wolfgang
APPLICANT: Matzku, Siegfried
TITLE OF INVENTION: Immunoconjugates II
5: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%;
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Best Local Similarity 75.0
Matches 3; Conservative
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                            STREET: One P
CITY: Boston
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    ADDRESSEE:
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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OTHER INFORMATION: Cyclicized modulating agent comprising
TOTHER INFORMATION: desmoglein-1 cell adhesion recognition sequence
US-09-535-852-1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
ITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
ITTLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: PastSEQ for Windows Version 4.0
IENGTH: 5
                                                                                                                                                                                                                                                                             APPLICANT: Lockhart et al.
APPLICANT: Lockhart et al.
APPLICANT: Lockhart et al.
TITLE OF INVENTION: Identification of Molecular Sequence;
TITLE OF INVENTION: Synatures in Nucleic Acid Molecules
FILE REFERENCE: 3016.2
CURRENT APPLICATION NUMBER: US/09/321,481
CURRENT APPLICATION NUMBER: 08/933,219
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 5
100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%; Score 14; DB 4; Length 5; 50.0%; Pred. No. 4.1e+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.3%; Score 14; DB 3; Length 5; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Synthetic Sequence
OTHER INFORMATION: Synthetic Sequence
US-09-321-481-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-535-852-1028
; Sequence 1028, Application US/09535852
; Patent No. 6638911
                                                                                                                                                                           RESULT 14
US-09-321-481-2
'Sequence 2, Application US/09321481
'Patent No. 6391550
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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RALD 5
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Search completed: May 26, 2005, 19:59:55 Job time : 41 secs This Page Blank (uspto)

5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2005 Copyright

protein search, using sw model OM protein - Run on:

May 26, 2005, 20:08:51; Search time 39 Seconds (without alignments) 29.605 Million cell updates/sec

US-10-047-945-4 69 Title: Perfect score:

1 LKAMDPTPPLWI 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

1582 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 12 88 Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
-	27	39.1	7	~	A61081	tryptophyllin, bas
7	27	39.1	10	~	A36454	trypsin-modulating
٣	24	34.8	80	0	S21288	lectin - potato (f
4	23	33.3	7	4	A58725	xin
ß	21		10	N	C35389	urease (EC 3.5.1.5
9	21	30.4	1.0	~	B59272	peptide-N4-(N-acet
. 1	21	30.4	10	~	839030	lysyl-bradykinin -
ω	21	30.4	11	Н	XAVIBH	bradykinin-potenti
σ	20	29.0	S	~	B60274	major protein anti
10		29.0	80	N	S10783	enamelin f - bovin
11	20	29.0	8	~	A39308	glycine reductase
12		29.0	12	Н	JIJG0	tremerogen A-10 -
13		29.0	12	0	PN0663	dystrophin-associa
14	19	27.5	6	~	B30572	T-cell receptor be
15	19	7	σ	7	A60108	exotoxin A - Strep
16	19	•	σ	~	S26508	collagen alpha 2(V
17	19	27.5	10	~	C30572	T-cell receptor be
18	19	27.5	11	N	D45900	complement C3b rec
19	18	26.1	4	7	151049	metallothionein-A
20	18	26.1	œ	7	S71919	alcohol dehydrogen
21	18	26.1	10	~	PC2171	triacylglycerol li
22	18		10	~	A61007	hementin (EC 3.4
23	18	26.1	11	7	C61497	seed protein ws-18
24	18	26.1	12	7	A49033	T-cell receptor de
25	18	26.1	12	~	JQ2308	hypothetical 1.4K
56	18	26.1	12	~	JQ2318	hypothetical 1.4K
27	18	26.1	12	~	158273	thyroglobulin - ra
28	18	26.1	12	0	S07436	tachykinin - Afric
53	17	24.6	7	7	809652	hypothetical prote

leucokinin VII - M alpha-gliadin 4Ha	alpha-gliadin 6Ha beta-glucosidase ( microbial collagen	napin small chain Ig H chain V-D-J r Ig H chain V-D-J r	ATP synthase D cha lebetin 1 isoform acid proteinase li	adipokinetic hormo acylase - Kluyvera	gene c-mpl protein ATPase Rl subunit
JS0317 A61218	B61218 PQ0231 A26093	S70337 PH1587 PH1611	PN0046 S71380 B37988	S10596 S19288	A31370 I58350 D48186
000	0 0 0	0 0 0	0 0 0	000	100
8 0 5	17 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	222	12 12 5	<b>co</b> co c	0 0 0
24.6	24.6 24.6 24.6	24.6 24.6 24.6	24.6 24.6 23.2	23.5	23.5
17	17	17	17 17 16	16	16 16
30	3 3 3 3 4 4	35 37	8 8 8 8 6 0	444	4 4 4 ህ 4 7

## ALIGNMENTS

		leaf
		Rohde's
		1
		basic
ULT 1	.081	Totophyllin,

tryptophyllin, basic - Rohde's leaf frog C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61081
R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
R;Montecucchi, Protein Res. 33, 391-395, 1989
A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containi A;Reference number: A61081
A;Accession: A61081

A Molecule type: protein
A, Residues: 1-7 < AMON.
A, Residues: 1-7 < AMON.
C, Comment: The biological activity of this peptide was not determined.
C, Superfamily: unassigned animal peptides
C, Seywords: amidated carboxyl end; hydroxyproline; skin
F;3/Modified site: 4-hydroxyproline (Pro) #status experimental
F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Gaps . 0 1; Indels Length 7; Score 27; DB 2; I Pred. No. 2.8e+05; 0; Mismatches 1; Query Match 39.1%; Best Local Similarity 80.0%; Matches 4; Conservative (

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8 PPLWI 12 PPSWI 6 ઠે 셤

trypsin-modulating oostatic factor - yellow fever mosquito

C.Species: Aedes aegypti (yellow fever mosquito) C.Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

A; Accession: A36454

A; Molecule type: protein A; Residues: 1-10 <BOR>

A;Cross-references: UNIPROT:P19425
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A;Reference number: A61630; MUID:93357794; PMID:8353526

A;Molecule type: protein A;Residues: 1-10 <B02>

A, Description: inhibits systhesis of trypsin- and chymotrypsin-like enzymes by midgut ep A; Note: none of the amino acids is modified C; Function:

Gaps

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C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C35389
K;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Reference number: A35389; MUID:90264298; PMID:2345135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide-NA-(N-acetyl-beta-glucosaminyl)asparagine amidase (BC 3.5.1.52) A, small chain - N;Alternate names: peptide N-glycosidase S;Species: Prunus dilcis var. sativa (sweet almond) C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004 C;Accession: B59272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A. A, Reference number: A59272; MUID:98181894; PMID:9523720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiConlon, J.M.; Olson, K.R.
PEBS Lett. 334, 75-78, 1993
A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A;Reference number: S39030; MUID:94039817; PMID:8224232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lysyl-bradykinin – rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiAltmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K. Bur. J. Biochem. 252, 118-123, 1998
A; Title: Characterisation of peptide-N4-(N-acetyl-bet
                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 2;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA-
A;Cross-references: UNIPROT:P17339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 -AAIT>
A;Cross-references: UNIPROT: P81898
C;Keywords: hydrolase
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66.7%;
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Best Local Similarity 75.v.
3; Conservative
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A,Molecule type: protein
A,Residues: 1-10 <CON>
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nes 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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MQLTPP 6
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Riwillar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1822
A.Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizatio
A; Reference number: S21289; MUD:92272683; PMID:1590771
A; Accession: S21286
A; Molecule type: protein
A; Residues: 1-8 < MIL>
A; Residues: 1-8 < MIL>
A; Cross-references: UNIPROT:Q7MIV6
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Species: Amanita virosa (destroying angel)
C;Accession: AS8725
R;Faulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A;Reference number: A58725; MUID:6893271; PMID:6893271
A;Accession: A58725
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <FAU>
C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide
F;2/Modified site: D-threonine (Thr) #status experimental
F;2/Modified site: D-threonine (Thr) #status experimental
F;3/Modified site: D-threonine (Thr) #status experimental
F;4/Modified site: 2-methylsulfonylkryptophan (Trp) #status experimental
F;7/Modified site: 2-methylsulfonylkryptophan (Trp) #status experimental
F;7/Modified site: 2-methylsulfonylkryptophan (Trp) #status experimental
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                                                                                                                                                                                                                                                                                                             lectin - potato (fragment)
C.Species: Solanum tuberosum (potato)
C.Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C.Accession: S21288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 4; Length 7;
Pred. No. 2.8e+05;
1; Mismatches 2; Indels
                                                                                                1; Indels
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                                            39.1%; Score 27; DB 2; I ilarity 80.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 1;
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Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
                                            Query Match
Best Local Similarity
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2 ASTPSPP 8
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C; Keywords: hormone
                                                                                                  4.
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J. Biol. Chem. 266, 22147-22153, 1991
A; Hitle: Glycine reductase protein C. Properties and characterization of its role in than Reference number: A39308; WUID:92042141; PMID:1939235
A; Accession: A39308
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tremerogen A-10 - jelly fungus (Tremella mesenterica)
C;Species: Tremella mesenterica
C;Dete: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01642; A61313
R;Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
Science 212, 1525-1527, 1981
A;Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-12 <SAKI>
A; Cross-references: UNIPROT: P01371
A; Cross-references: UNIPROT: P01371
A; Note arnesyl may instead be (2E, 6E, 102) -12-hydroxyfarnesyl
B; Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.
Agric. Biol. Chem. 42, 1301-1302, 1978
A; Title: Amino acid sequence of tremerogen A-10, a peptidal hormone, inducing conjugatic
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A;Residues: 1-12 <SAK2>
C;Comment: Tremerogen A-10 is produced by the A mating-type cells and induces formation
C;Superfamily: tremerogen a-13
C;Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; pheror
F;12/Binding site: farnesyl (Cys) (covalent) #status experimental
F;12/Modified site: methyl ester carboxyl end (Cys) #status experimental
                                                                                                                                                                                                         sulfhydryl protein C, alpha chain - Clostridium stickla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: glycine reductase complex catalyzes the reductive deamination of glycine C; Keywords: ATP; oxidoreductase
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                                                                                                                                                                                                  glycine reductase (BC 1.4.99.-) sulfhydryl protein C, alpha chain - Clostric
C,Species: Clostridium sticklandii
C,Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
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Pred. No. 2.8e+05;
0; Mismatches 1;
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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Stadtman, T.C.; Davis, J.N.
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                                                        2 PLPP 5
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PTPP
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                                                                                                                             Cipecies: Agkistrodon halys (halys viper)
Cipate: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
Cipate: 30-Sep-1985
Cipate: 319-342, 1985
Affile: Structure-function studies on the bradykinin potentiating peptide from Chinese A; Accession: JC0002, MUID:86177022; PMID:3008123
A; Accession: JC0002
A; Comment: Because this peptide both inhibits the activity of the angiotensin-converting C; Superfamily: bradykinin-potentiating peptide
C; Superfamily: bradykinin-potentiating peptide
C; Superfamily: bradykinin-potentiating peptide
C; Superfamily: bradykinin-potentiating enzyme inhibitor; antihypertensive; bradykinin; pyrog
C; Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical matigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Bate: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
R;Magai, S; Wiker, H.G; Harboe, M.; Kinomoto, M.
R;Magai, S; Wiker, H.G; Harboe, M.; Kinomoto, M.
R;Magi, S; Wiker, H.G; Harboe, M.; Kinomoto, M.
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Reference number: A60274; Ailoin antigens in the culture A;Status: preliminary
A;Residues: 1-5 «NAG»
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C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Accession: 810783
R.Strawich, E.; Glimcher, M.J.
Bur. J. Blochem. 191, 47-56, 190
A.Title: Tooch 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: 810780; MulD:9033641; PMID:2379503
A,Accession: 810783
A,Accession: 810783
A,Holecule type: protein
A,Residues: 1-8 <STR>
C.Keywords: enamel; phosphoprotein
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
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Pred. No. 1.3e+03;
1; Mismatches 1;
                                                                              bradykinin-potentiating peptide - halys viper
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75.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                 Alternate names: BPP
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Search completed: May 26, 2005, 20:18:24
Job time : 41 secs
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N.Alternate names: blastogen A; scarlet fever toxin

N.Alternate names: blastogen A; scarlet fever toxin

S.Species: Streptococcus pyogenes

C; Bate: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

R; Schlievert, P.M.; Gray, E.D.

N.Schlievert, P.M.; 1865-1867, 1989

A.Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast A; Reference number: A60108; MUID:89254013; PMID:2498210

A; Molecule type: protein

A; Molecule type: protein

A; Residence: 1-9 *SCH->

A; Residence: 1-9 *SCH->

A; Residence: 1-9 *SCH->

A; Coss-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNIFCC; Keywords: exotoxin
dystrophin-associated glycoprotein Ala-II - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0663
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Yitle: A dystrophin-associated glycoprotein, Ala (one of 43DAG doublets), is retained A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Accession: PN0663
A;Accession: PN0663
A;Accession: I-12 <VOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: glycoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: B30572
R, Williams, C.B.; Gutman, G.A.
R, Williams, C.B.; Gutman, G.A.
A; Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz A; A; Accession: B30572
A; Accession: Preliminary; not compared with conceptual translation
A; Accell type: MRNA
A; Molecule type: MRNA
A; Residues: 1-9 < WIL.>
C; Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain C region (CRTB29) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
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Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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GenCore version 5.1.6
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protein search, using sw model ı OM protein

May 26, 2005, 20:00:51 ; Search time 171 Seconds (without alignments) 35.935 Million cell updates/sec Run on:

US-10-047-945-4 69

1 LKAMDPTPPLWI 12 score: Perfect sc Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

4233 Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

seq length: 0 seq length: 12 88 Minimum Maximum 1 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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<u>.</u>		pachymedusa	aedes aegyp	homo sapien	canis fami]	acinetobact	solanum tub	eurypharynx	homo sapien	maripa pani	maripa repe	wilsonia hu	seddera hir	odonellia	aniseia arg	merremia pe	ipomoea alb	litoria rub	homo sapien	chlamydomon	pseudomonas	lepisosteus	oncorhynchu	prunus dulc	morganella	klebsielja	agkistrodon	oreochromis	escherichia	mus musculu	clostridium	rattus sp.
2000	T TOOD T	P83455	P19425	Q9ucr1	Q6x7v1	Q8kz86	Q7m1v6	Q76mk5	Q8ivg8	Q8maz1	Q8maz3	Q8mb39	Q8mb58	Q8mb77	Q8mb79	Q8mb97	Q8mbe1	P82096	Q9h326	Q6sp94	099193	09prj4	Q9prz1	P81898	P17339	Q67bk2	P04562	077896	047251	P38642	Q7m010	Q91wz3
			TMOF_AEDAE	Q9UCR1	Q6X7V1	Q8KZ86	Q7M1V6	Q76MKS	Q8IVG8	Q8MAZ1	Q8MAZ3	Q8MB39	Q8MB58	Q8MB77	Q8MB79	Q8MB97	Q8MBE1	EI01_LITRU	<u> 0</u> 9н3 <u>2</u> 6	Q6SP94	099193	Q9PRJ4	BRK_ONCMY	PNAS_PRUDU	URE3_MORMO	Q67BK2	BPP_AGKHP	077896	047251	UF04 MOUSE	Q7M0L0	Q91WZ3
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& Query Match	Hacen	39.1	39.1	37.7	36.2	36.2		33.3	33.3	31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.9	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	σ	29.0	29.0
o co		27	27	26	25	25	24	23	23	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21	21	20	20	20
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Q75595 human immun Q9hcn5 homo sapien P01371 tremella me			P83278 macrobrachi P40930 homo sapien Q8vhm9 mus musculu Q9esu5 mus musculu
Q75595 Q9HCN5 TA10 TREME	Q9BZ49 Q7YNG6 Q6LDP8	Q9ET16 Q9ET17 Q9ET18 Q7M2M9	FARS_MACRS UHA3_HUMAN Q8VHM9 Q9ESUS
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# ALIGNMENTS

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-1- TISSUE SPECIFICITY: Skin.
-1- MASS SPECIFICITY: Skin.
-1- MASS SPECIFICITY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
-0. GO: OG:005576; C:extracellular; NAS.
GO: GO:0045986; P:negative regulation of smooth muscle contra...; NAS.
Amidation, Amphibian defense peptide; Direct protein sequencing;
Hydroxylation.
                                                                                                                                                                       [1] -SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                   TISSUE=Skin secretion;
Chen T.B., Orr D.F., Shaw C.;
"Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
                                                                                                                 Euteleostomi;
Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                              Tryptophyllin-1 (PdT-1).

Pachymedusa dacnicolor (Giant mexican leaf frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Bukaryota; Matazoa; Anura; Neobatrachia; Hyloidea; Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                      3 3 Hydroxyproline.
7 7 Proline amide.
7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.1%; Score 27; DB 1; 1 60.0%; Pred. No. 1.6e+06; tive 1; Mismatches 1;
                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                 7 AA.
                  PRT;
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Best Local Similarity 60.0
Matches 3; Conservative
                  STANDARD;
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                  PACDA
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MOD RES
SEQUENCE
                  TPFY PA P83455;
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 45, Last annotation update)
Trypsin-modulating owstatic factor (TMOF) (OOSH).
Aedes aegypti (Yellowfever mosquito).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota; 10 AA. PRT; STANDARD; TMOF AEDAE P19425; TWOF AEDAE

ID TWOP AE

AC 01-107

DT 01-10V

DT 25-0CT

DE 75-0CT

DE 75-0CT

OS Aedes 6

OC Eukary RESULT 2

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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDILINE=22929740; Pubmed=12890727; Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.; Isolation and expression analysis of the canine insulin-like factor 3
                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Moraxellaceae, Acinetobacter.
NCBI_TaxID=470;
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Pred. No. 2.5e+03;
0; Mismatches 4; Indels
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                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.";
Biol. Reprod. 69:1658-1664(2003).
EMBL, AX251015; AAP79519.1; -.
NON TER 12
SEQÜENCE 12 AA; 1354 MW; 20ED
                                                                                                                                                                                                                                                                                           Insulin-like factor 3 (Fragment).
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                                                                                                                                             Q6X7V1;
05-JUL-2004
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                                                                                                                                                                           STRAIN=Vero beach; TISSUE=Cvary; MEDLINE=90367888; PubMed=2394318; Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.; Wosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut."; PASEB J. 4:3015-3020(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development.

DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs and stops at 56 hrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Vero beach; TISSUE=Ovary;
MEDLINE=93357794; PubMed=835526; DOI=10.1016/0965-1748(93)90044-S;
MEDLINE=93357794; PubMed=835526; DOI=10.1016/0965-1748(93)90044-S;
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MEDCINE=93357794; STRAINE TO THOTO TO THE TARGET TO THE TARGET
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=92129337; PubMed=1733949;
MEDLINE=92129337; PubMed=1733949;
Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V., Schiffmann E., Liotta L.A.;
"Identification, purification, and partial sequence analysis of autocaxin, a novel motility-stimulating protein.";
J. Biol. Chem. 267:2524-2529(1992).
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBI_TaxID=7159;
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Pred. No. 9.7e+02;
0; Mismatches 1; Indels
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YD -> DY (in TMOF(B)).
236D0A7777776DC7 CRC64;
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Direct protein sequencing; Hormone.
DOMAIN 3 10 Poly-P
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MEDLINE-22270987; PubMed=12384388; Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E., Monti-Bragadin C., Lavenia A., Dolzani L.; Monti-Bragadin C., Lavenia A., Dolzani L.; Wolecular characterization of integrons in epidemiologically unrelated clinical isolates of Acinetobacter baumannii from Italian hospitals reveals a limited Ddversity of gene cassette arrays."; Antimicrob. Agents Chemother. 46:3665-3668 (2002).

ENBL; AJ313334; CAC85941.1; -.
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01-MAR-2004 (TrEMBLrel. 26, Created)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Convolvulaceae; Maripeae; Maripa.
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"Monophyly of the Convolvulaceae and circumscription of their major
lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
BMBL; AX100937; AAM55689.1; -.
GO: GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuett H.C., Herz J., Stanley K.K.;
"Structure of the low-density lipoprotein receptor-related protein
                                                                                                                                                                                                          Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Low density lipoprotein receptor related protein [Lipoprotein receptor related protein]
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o. 4.7e+03; Indels
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. ...
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MBBL; Y18524; CAD57168.1; -
EMBL; X18424; CAA33464.1; -
GO: GO:0004872; F:receptor activity; IEA.
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MEDLINE=90089395; Pubmed=2597675;
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SEQUENCE 11 AA; 122
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                                   Lectin (Fragment)
Solanum tuberosum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids; Solanales; Solanaceae; Solanum.
VCBI_TAXID=4113;
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Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
                                                                                                                                                                                                                                                           Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R., Bolwell G.P., "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 283:813-821(1992).
PIR; S21288; S21288.
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Pred. No. 4.3e+03;
2; Mismatches 0; Indels
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SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL, AY100897, AAM55711.1; -.
GO, GO:0009507, C:chloroplast; IEA.
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11 AA; 1260 MW;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Maripeae; Maripa.
NCBI_TaxID=197412;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Cresseae; Wilsonia.
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Stefanovic S., Krueger L., Olmstead R.G.;
Monophyly of the Convolvulaceae and circumscription of their major lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522(2002).
EMBL; AY100936; AAM55865.1; -..
GO; GO:0009507; C:chloroplast; IEA.
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Stefanovic S., Krueger L., Olmstead R.G.;
Stefanovic S., Krueger L., Olmstead R.G.;
Wonophyly of the Convolvulaceae and circumscription of their major lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 99:1510-1522 (2002).
EMBL; AY100914; AAM55771; -.
GO; GO:0009507; C:chloroplast; IEA.
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lamiids; Solanales; Convolvulaceae; Cresseae; Seddera.
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"Monophyly of the Convolvulaceae and circumscription of their m:
lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522(2002).
EMBL; AX100905; AAM55743.1; -.
GO; GO:000557; C:chloroplast; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Stefanovic S., Krueger L., Olmstead R.G.;
"Monophyly of the Convolvulaceae and circumscription of their major lineages based on DAN sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
BMBL; AY100895; AAM55703.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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Stefanovic S., Krueger L., Olmstead R.G.;
"Monophyly of the Convolvulaceae and circumscription of their major lineages based on DNA sequences of multiple chloroplast loci.";
Am. J. Bot. 89:1510-1522 (2002).
EMBL; AX100885; AAM55663.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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NON TER 11 11
SEQÜENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
PSDJ (Fragment)
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Best Local Similarity
Matches 3; Conserv
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Chloroplast.
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PLW 11
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Search completed: May 26, 2005, 20:17:51 Job time : 185 secs

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protein search, using sw model OM protein Run on:

May 26, 2005, 20:00:02; Search time 159 Seconds (without alignments) 29.189 Million cell updates/sec

US-10-047-945-4 69 score: Title: Perfect :

1 LKAMDPTPPLWI 12 **BLOSUM62** Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

520583

seq length: 0 seq length: 12 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp2002s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

u	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic	Synthetic	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Human can	Hydroxyme	Human can	Human can	Human can	Human 213	Human can	Human can	Human can	Human can
Description	Abb80225 8	Abb80226 S	Aaw53843 1	Abb80222 S	Abb80227 8	Abb80228 8	Abr12621 B	Abr12017 B	Abr12854 B	_	Abr11875 B	Abr12121 F	Abr12948 F	Abr12106 B	Abr12294 F	Abr12738 F	Aaw21252 F	Abr11778 B	Abr12206 B	Abr12924 F	Ado64358 F	Abr12770 B	Abr12969 B	Abr12458 F	Abr12601 F
ΩI	ABB80225	ABB80226	AAW53843	ABB80222	ABB80227	ABB80228	ABR12621	ABR12017	ABR12854	ABR12743	ABR11875	ABR12121	ABR12948	ABR12106	ABR12294	ABR12738	AAW21252	ABR11778	ABR12206	ABR12924	AD064358	ABR12770	ABR12969	ABR12458	ABR12601
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% Query Match	100.0	94.2	78.3	78.3	72.5	62.3	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	55.1	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2
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# ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. ABB80225 standard; peptide; 12 AA. 06-NOV-2003 (first entry) Synthetic LTNF, LT-12. ABB80225; ABB80225 

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

e.g. Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgB levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

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arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
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                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                          100.0%; Score 69; DB 7; Length 12; 100.0%; Pred. No. 0.00033;
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                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 ABB80226 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                         1 LKAMDPTPPLWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic LINF, LT-11
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                                                                                                                                                                             Sequence 12 AA;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Garaves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by

Claim 7; Page 4; 24pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
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                                                                                                                                                          Score 65; DB 7; Length 11,
Pred. No. 0.0013;
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100.0%; Pred. No. v...
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                                                                                                                                                                                                                                                                                                                                                                   AAW53843 standard; peptide; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histamine reaction treatment.
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94US-00310340.
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                                                                                                                                                                                          Local Similarity 100.
nes 11; Conservative
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                                                                                                                                                                                                                                                                               1 LKAMDPTPPLW 11
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                                                                                                                                            Sequence 11 AA;
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(LIPP/) LIPPS
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22-SEP-1994;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTME) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), insure growth factor (NGF), insulin, myoglobin and/or adenosinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum. Saliva proteins
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                   ö
                  Length 10;
                                                   0; Indels
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                 Score 54; DB 2;
Pred. No. 0.067;
0; Mismatches 0
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                  78.3.,
100.0%; Pr
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                                                   Conservative
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                                                                                                     LKAMDPTPPL 10
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     saliva; ELISA.
                                                                                                                                                                                                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                   ABB80222;
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                                                                                                                                                                  RESULT 4
                                                                                                                                                                                 ABB80222
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & [1g5], nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva callection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifuged immediately, whereas blood requires
                                                                                                                                                                                                                                                                                       Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid archritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06;
                                                                                                                                   ABB80227 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 4; 24pp; English.
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                                                                                                                                                                                                              06-NOV-2003 (first entry)
10
                    1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                      Synthetic LINF, LT-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipps BV, Lipps FW;
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LKAMDPTPPL
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003060471-A2.
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                                                                                                                                                                                                                                                                                                                                                                                            saliva; ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                          ABB80227;
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                                                                                                                   ABB80227
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Indels

100.0%; Pred. No. 1.8 ive 0; Mismatches

Conservative

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Gaps

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78.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.067; ive 0; Mismatches 0; Indels

10; Conservative

Query Match Best Local Similarity Matches 10; Conserv

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insurin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, attoimmune an endorman and an endorman perfection or the protein may be monitored by assaying a human endogenous protein by performing an enti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple BLISA test, whereas an assay of proteins from a be assayed by a simple BLISA test, whereas an assay of proteins from requires a more complicated sandwich type BLISA
                                                                                                                                                                                                                                                       Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                 ABB80228 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 4; 24pp; English.
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                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                     Synthetic LINF, LT-8.
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Best Local Similarity
Matches 8; Conserv
1 LKAMDPTPP
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saliva; ELISA.
                                                                                                                                                                                06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                              vaccine; cancer; immune response; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.4%; Score 41; DB 6; Length 9; 66.7%; Pred. No. 1.8e+06; ive 2; Mismatches 1; Indels
                                                                                                              Human cancer-related protein 156P1D4 HLA peptide #856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Morrison RK, Raitano AB;
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               ABR12621 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Challita-Eid PM,
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                            Human; cytostatic; vacci
human leukocyte antigen.
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1 MDPSVPIWI
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                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                             24-OCT-2002.
                                               ABR12621;
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ID ABR
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ABR12621
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10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                     (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                   from the invention
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                                                                                               Jakobovits A,
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                                                                                                              Morrison K,
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                   New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                   Ge W, Hubert RS;
Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 6; Length 9; Pred. No. 1.8e+06; Mismatches 1; Indels
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                                                                                                                                                                                                                                  Jakobovits A, Challita-Eid PM, Faris M,
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 232; 1021pp; English.
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25-APR-2001; 2001US-0286630P.
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Best Local Similarity
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MDPSVPIWI
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                                         Homo sapiens
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transcripts, and
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                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human cancer-related genes and proteins (ABZ7810-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humaral or cellular immune response. The genes are useful a probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                     modulates the structure
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   Hubert RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; vaccine; cancer; immune response; HLA;
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Ge ₩,
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Pred. No. 1.8e+06;
                                                                                                                                                                     composition comprising a substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
   Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Challita-Eid PM, Faris M,
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Morrison K, Morrison RK, Raitano AB;
                                   Morrison RK, Raitano AB;
                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 240; 1021pp; English.
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Challita-Eid PM
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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RESULT 12
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                                                                                                                                                                                                                                 proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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                                                                     proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
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                                                                                                                                                                                                                  present invention relates to novel human cancer-related genes and
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                                                 composition comprising a substance that modulates the structure
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Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jakobovits A, Challita-buc ...,
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                                                                                                                                                                Claim 13; Page 239; 1021pp; English.
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25-APR-2001; 2001US-0286630P.
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Matches 6, Conservative
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WPI; 2003-075555/07
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                                                                                                                    cancer patients
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The present invention relates to novel human cancer-related genes and

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             The genes are useful as probes and primers for cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or thair fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer-related protein 156P1D4 HLA peptide #356.
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                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                         Score 41; DB 6
Pred. No. 7.9;
2; Mismatches
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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MDPSVPIWI
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                                     Sequence 10 AA;
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vaccine; cancer; immune response; HLA;
                                                                                                                                                                               Human cancer-related protein 156P1D4 HLA peptide #341.
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Morrison RK, Raitano AB;
                                                                               ABR12106 standard; peptide; 10 AA.
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25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                             human leukocyte antigen.
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    1 MDPSVPIWI 9
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                                                                                                                                                                                                             cytostatic;
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                                                                                                                                                                                                              Human;
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Matches
                                                   RESULT 14
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                                                                  ABR12106
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                                                                                                                                                                                                                                                                                                                                                                       Human; cytostatic; vaccine; cancer; immune response; HLA;
                                                                6; Length 10;
                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                       Human cancer-related protein 156P1D4 HLA peptide #1183.
                                                              Score 41; DB 6
Pred. No. 7.9;
                                                                                            2; Mismatches
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Morrison K, Morrison RK, Raitano AB;
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                                                                                                                                                                                                                                         ABR12948 standard; peptide; 10 AA.
                                                              59.4%;
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25-APR-2001; 2001US-0286630P.
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MDPSVPIWI 9
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                                                             Query Match
Best Local Similarity
Matches 6; Conserv
from the invention
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                                  Sequence 10 AA;
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ABR12948
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Hubert RS;

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Faris M,

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New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                             The present invention relates to novel human cancer-related genes and
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                                                                                                                                                                                                            Claim 13; Page 233; 1021pp; English.
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MDPTPPLWI 12

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or callular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                            Hubert RS;
                                                   Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.
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                  Human cancer-related protein 156P1D4 HLA peptide #529.
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Morrison K, Morrison RK, Raitano AB;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                         Homo sapiens
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Gaps .. 0

6; Conservative

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May 26, 2005, 20:18:00 ; Search time 134 Seconds (without alignments) 30.893 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/RCT7_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1462099 seqs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKAMDPTPPLWI 12
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69
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                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c	4, Appli	'n	1, Appli	9	7, 1	25	735,	6, Appli			188, App	168,	168, App
Description	Sequence 4,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES ID	US-10-047-945-4	US-10-047-945-5	US-10-047-945-1	US-10-047-945-6	US-10-047-945-7	US-10-930-300-52	US-10-327-598-735	US-10-185-815-6	US-10-161-791-252	US-10-116-275-52	US-10-611-440-188	US-10-437-708-168	US-10-418-032-168
	14	14	14	14	14	17	16	14	14	12	16	15	17
% Query Match Length DB	12	11	10	Q	80	0	12	12	12	12	0	80	80
% Query Match	100.0	94.2	78.3	72.5	62.3	55.1	49.3	46.4	46.4	46.4	44.9	43.5	43.5
Score	69	65	54	20	43	38	34	32	32	32	31	30	30
Result No.	-	7	m	4	ı,	9	7	æ	60	10	11	12	13

Sequence 480, App Sequence 165, App Sequence 2288, App Sequence 27, Appli Sequence 7, Appli Sequence 10870, A Sequence 10923, A Sequence 10923, A Sequence 10923, A Sequence 74, Appl Sequence 74, Appl Sequence 74, Appl Sequence 619, App Sequence 619, App Sequence 619, App Sequence 619, Appl Sequence 619, Appl Sequence 619, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 273, Appl Sequence 274, Appl Sequence 274, Appl Sequence 274, Appl	Sequence 29, Appi Sequence 29, Appi
4 US-10-190-082- 5 US-10-437-708- 7 US-10-225-5673- 6 US-10-225-5673- 6 US-10-277-292- 7 US-10-277-475B 5 US-10-057-475B 5 US-10-057-475B 5 US-10-057-475B 5 US-10-057-475B 6 US-10-057-475B 7 US-10-154-884B 6 US-10-154-884B 7 US-10-154-884B 8 US-10-154-884B 8 US-10-154-884B 9 US-10-154-884B 10 US-10-154-884B 10 US-10-154-884B 10 US-10-185-817- 10 US-10-235-175- 10 US-10-	US-09-758-12
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	7 39.
4497 8 9 9 1 1 2 2 2 2 2 2 2 2 2 2 3 2 3 4 4 4 4 4 4 4	r 4 r C

# ALIGNMENTS

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; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4
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Sequence 4, Application US/10047945;
Sequence 4, Application US/10047945;
Publication No. US200301575551
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: (1gE) IMPLICATED DISORDERS;
TITLE OF INVENTION: 01650 IMPLICATED DISORDERS;
FILE REFERENCE: FWLPATO1508;
CURRENT FILING DATE: 2002-01-14;
PRIOR PILICATION NUMBER: US/10/047,945;
PRIOR FILING DATE: 2002-01-14;
PRIOR FILING DATE: 1002-01-14;
SOCTWARE: WORDPERFECT 5.1 FOR WINDOWS;
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 69; DB 14; Length 12; 100.0%; Pred. No. 0.00098; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 12, Conservative
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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                 Corresponds to fragment 1-9 of 2 above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E TITLE OF INVENTION: LIPPS, IMPLICANTED DISORDERS
TITLE OF INVENTION: LIPPS, IMPLICATED DISORDERS
TITLE OF INVENTION: LIPPS, IMPLICATED DISORDERS
TITLE REPERENCE: FWLLPATIONS: US/10/047,945
CURRENT APPLICATION NUMBER: US/10/047,945
FRICH FILING DATE:
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 6
LENGTH: 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10047945
; Publication No. US2030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, REDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: LIPPS, INVENTION: USPENDENCE: FILE REFERENCE: FULPATO15US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR PILING DATE: PROS-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.3%; Score 43; DB 14; Length 8; 100.0%; Pred. No. 1.3e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NESCUE 10-930-300-52
Sequence 52, Application US/10930300
Sequence 52, Application No. US20050014138A1
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: Synthetic. US-10-047-945-7
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LKAMDPTP 8
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corresponds to fragment 1-11 of 2 above.
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    US-10-047-945-5

Sequence 5, Application US/10047945

Publication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TILLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1gB) IMPLICATED DISORDERS

FILE REFERENCE: FWLPAT015US
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Sequence 1, Application US/10047945

Publication No. US20030157555A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: 0.146019518 AND TREATMENT FOR IMMUNOGLOBULIN ITLLE OF INVENTION: (19E) IMPLICATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 10; 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/047,945 CURRENT FILING DATE: 2002-01-14 PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54;
Pred. No.
                                                                                                                                                                                                                                                                       NUMBER OF SEQ 1D NOS: 7
SOFWMARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 5
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.2%; Sco...
100.0%; Pre
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; Sequence 6, Application US/10047945
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic.
US-10-047-945-5
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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LENGTH: 10
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Gaps
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                                                                                                                                                                                  Sequence 6, Application US/10185815;
Sequence 6, Application US/10185815;
Publication No. US20030086354A1
SEQUENCE INFORMATION:
APPLICANT: Elan Corporation, plc
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands;
TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands;
CURRENT APPLICATION UNMER: US/10/185,815
CURRENT FILING DATE: 2002-10-09
PRIOR FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.4%; Score 32; DB 14; Length 12; 100.0%; Pred. No. 3.5e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STANCE, AUGUST K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: 1SOLATING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
         ;
      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: polypeptide ligand US-10-185-815-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 252, Application US/10161791; Publication No. US20030186863A1; GENERAL INFORMATION: APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
      5; Conservative
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                                               2 KAMDPTPP
                                                                        :: ||||||
1 QSFDPTPP
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-161-791-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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Publication No. US20040181039A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Krah, Bugene
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawron, Robert
TITLE OF INVENTION: for Making and Using Them
FILE REPREBNCE: 01-799-A
FURRENT APPLICANTON WUMBER: US/10/327,598
CURRENT APPLICATION NUMBER: US 60/344,874
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR PILING DATE: 20002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
SEQ TWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY Disk, 3.50 inch, 1.44MB Storage COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-Aug-2004
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 16; Length 12; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.1%; Score 38; DB 17;
85.7%; Pred. No. 1.3e+06;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDENESS: single
TOPLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-322-737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                             NUMBER OF SEQUENCES: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.3%;
                                                                                                                           CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7°
....has 6; Conservative
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Best Local Similarity
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US-10-327-598-735
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APPLICANT: Kieliseseski, Marcia
APPLICANT: Kieliseseski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US/09/547,693
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
43.5%; Score 30; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 9;
1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 168, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: CLP-2825
US-10-611-440-188
Radvanyi, Laszlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 DPTPPLW 11
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ETSPPLW 8
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; OTHER INFORMATION: take Across the GIT"
US-10-116-275-52
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Publication No. US20030211476A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Branden, David
APPLICANT: Branden, David
APPLICANT: Branden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Genetic Analysis of Peyer's Patches and M Cells and Methods and TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
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                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 14; Length 12;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SSCTWARE: PatentIn version 3.1
LENGTH: 12
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Publication No. US20040197912A1
GENERAL INFORMATION:
APPLICANT: Berinstein, Neil
APPLICANT: Gallichan, Scott
APPLICANT: Parrington, Mark
APPLICANT: Parrington, Mark
APPLICANT: Pedyczak, Artur
US/08/602,999
                                                                                                1101-202
                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-2
RELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ IN NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                          46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
          FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                        ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-252
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KAMDPTPPL 10
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US-10-611-440-188
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Sequence 165, Application US/10437708
Publication No. US20040009555A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT APPLICATION NUMBER: US/09/547,693
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 165
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (5)...(6)
CTHER INFORMATION: The Proline at these positions is a hydroxyproline US-10-437-708-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(1) OTHER INFORMATION: The Proline at this position is a hydroxyproline. FEATURE: NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.5%; Score 30; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PTPPL 10
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                                                                                                          Sequence 168, Application US/10418032
Publication No. US20050074838A1
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: Glycoproteins
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: ONU-07775
CURRENT APPLICATION NUMBER: US/10/418,032
CURRENT PILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 274
SSEQ ID NO 168
LENGTH: 8
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1 LOCATION: (3)...(4)
2 OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-418-032-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.5%; Score 30; DB 17; Length 8; 100.0%; Pred. No. 1.3e+06; rive 0; Mismatches 0; Indels
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Publication No. US20030148264A1

GENERAL INFORMATION:

APPLICANT: Lasky, Lawrence A.

APPLICANT: Lasky, Lawrence A.

APPLICANT: Held, Heike A.

TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

FILE REFERENCE: P190511

CURRENT APPLICATION NUMBER: US/10/190,082

CURRENT FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic US-10-190-082-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 4; Conserva
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PTPPL 5
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                                                                                              US-10-418-032-168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Gaps

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ANTI-SENSE: NO
FRAGMENT TYPE: N
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HYPOTHETICAL: N
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165, App
18, Appl
7, Appli
2, Appli
2, Appli
2, Appli
12, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Appl
                                                                        May 26, 2005, 20:09:44; Search time 40 Seconds (without alignments) 22.395 Million cell updates/sec
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-652-877-31

US-08-652-877-31

US-09-500-114-252

US-09-532-4468-24

US-09-547-633-165

US-09-547-633-165

US-09-137-341-7

US-09-137-341-7

US-09-137-948-18

US-09-139-928-7

US-08-171-698-2

US-09-295-8468-15

US-09-295-948-12

US-09-251-738-12

US-09-251-738-12
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US-09-295-846B-16
US-09-551-737C-16
US-09-295-924B-3
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                       1 LKAMDPTPPLWI 12
                                                                                                                             US-10-047-945-4
69
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                                                                                                                                                                                                                                                                           seq length: 0 seq length: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match 1
                                                                                                                                             Perfect score:
                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                  OM protein
                                                                                                                                                          Sequence:
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                                                                             Run on:
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Appli
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Sequence 3, Ak
Sequence 3, App
Sequence 3.
              Sequence 4, At
Sequence 4, At
Sequence 4, At
Sequence 17, P
Sequence 17, P
Sequence 17, P
                                                                                                                            Sequence 11, 1
Sequence 11, 1
Sequence 7, Ap
                                                                                                     Sequence 14
Sequence 8,
US-09-551-738B-13

US-07-989-290-4

US-08-468-596-4

US-09-295-996B-14

US-09-295-96B-14

US-09-295-94B-4

US-09-551-737C-17

US-09-551-738B-14

US-09-551-738B-14

US-09-551-738B-14

US-09-551-738B-8

US-09-551-738B-8

US-09-551-738B-8

US-09-551-738B-8

US-09-551-738B-8

US-09-393-941-3

US-09-393-941-3

US-09-393-941-3

US-09-393-941-3

US-08-177-3
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## ALIGNMENTS

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Sequence 2, Application US/08657163A

| Sequence 2, Application US/08657163A
| Patent No. 574449
| GENERAL INFORMATION:
| APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
| TITLE OF INVENTION: SYNTHETIC LINPS AND THEIR
| TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS: ADDRESSEE: BINIE V. LIPPS
| STREET: 4509 MIMOSA DR. |
| CITY: BELLAIRE |
| STATE: TEXAS |
| COUNTRY: USA |
| COUNTRY |
| COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: RANDALE FORM:
WEDIUM TYPE: 35" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: CLASSIFICATION 514
PRIOR APPLICATION S14
PRIOR APPLICATION S14
CLASSIFICATION 1914
APPLICATION WHERE: 08/310,340
FILING DATE: 2 SEPTEMBER 1994
CLASSIFICATION WHERE: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 28,198
REFERENCE/DOCKET NUMBER: 28,198
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 713-463-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FI
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STRANDEDNESS:
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US-08-476-515A-31
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  APPLICANT:
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APPLICANT: Ullrich, Axel

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: U.S.A.
STATE: New York
COUNTRY: U.S.A.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: NEW AND-1994
CLASSIFICATION: 435
MAND: CONTACT TOWN NUMBER: US/08/336,343A
MAND: CONTACT TOWN NUMBER: US/08/336,343A
MAND: AND TOWN TOWN NUMBER: US/08/336,343A
MAND: AND TOWN TOWN NUMBER: US/08/336,343A
MAND: AND TOWN TOWN TOWN NUMBER: US/08/336,343A
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                                       Score 54; DB 1; Length 10; Pred. No. 0.011; 0; Indels
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                                         78.3%; Scc. No. ... 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                          US-08-336-343A-31
; Sequence 31, Application US/08336343A
; Patent No. 5677144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08652877 Patent No. 6187548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
SYNTHETIC
                                             Ouery Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                         1 LKAMDPTPPL 10
                                                                                                                                                                               1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-336-343A-31
    ; ORIGINAL SUI
US-08-657-163A-2
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Gaps
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APPLICANT: Akerstron, Goran
APPLICANT: Crumley, Greeg R.
APPLICANT: Crumley, Greeg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Hyalm, Goran
APPLICANT: Hyalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSER: Martin Savitzky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments TITLE OF INVENTION: Thereof and DNA Encoding Same NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
46.4%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 2CT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION NUMBER: US 08/344,836
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 31, Application US/08476515A; Patent No. 6239270
                                                                                                                       STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,699
REGISTRATION NUMBER: 29,699
REPERENCE/DOCKET NUMBER: A1
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-454-3816
                                                                                                                                         CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KAMDPTPPL 10
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Gaps
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Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: STORE, James B.
TITLE OF INVENTION: 1SOLATING AND WETHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
      COMPLUE. COMPLES. Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT G SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lefalie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
TELEPHONE: CALLA PERNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 3;
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-207
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide
US-08-602-999A-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SH
TITLE OF INVENTION: ISON
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KPMPPRPPL 12
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-500-124-252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
                                                                         COUNTRY: USA

ZIP: 19426-0107

ZIP: 19426-0107

ZIP: 19426-0107

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARR: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1994
PRIOR APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTONEX/AGENT INFORMATION:
NAME: SAVILSKY, MATTIN
REGISTRATION NUMBER: 29,699
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRANE: 610-454-3806
TELEBRANE: 610-454-3806
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 252, Application US/08602999A Patent No. 6184205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPARKS, Andrew B.
KAY, Brian K.
THORN, Judith M.
QUILLIAM, Lawrence A.
DER, Channing J.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 11 amino acids TYPE: amino acid STRANDEDNESS:
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                      Collegeville
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SPARKS
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GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT PAPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
FILE REFERENCE: 2183-4086US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 9201593.3
PRIOR APPLICATION NUMBER: EP 98201693.3
                                                                                                             ; LOCATION: (3)...(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i. LOCATION: (5)...(6); OTHER INFORMATION: The Proline at these positions is a hydroxyproline. US-09-547-693-165
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (3)..(3)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
                                              LOCATION: (1)..(1) OTHER INFORMATION: The Proline at this position is a hydroxyproline.
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82;
                                                                                                                                                                                                      43.5%; Score 30; DB 4; Length 8; 100.0%; Pred. No. 4.1e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.5%; Score 30; DB 100.0%; Pred. No. 82; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09315926A Patent No. 6498027 GENERAL INFORMATION: APPLICANT: ES van, Helmuth APPLICANT: Havenga, Menzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165, Application US/09547693
Patent No. 6639050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial/Unknown
    OTHER INFORMATION: Synthetic
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
5; Conserve
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                                                                                             NAME/KEY: SITE
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Patent No. 6639050

GENERAL INFORMATION:
APPLICANT: K. Aleliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 168
LENGTH: 8
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US-09-232-446B-24

i Sequence 24, Application US/09232446B

i Patent No. 6228647

i GENERAL INFORMATION:

i APPLICANT: VOYEAS, Daniel F.

i APPLICANT: Gai, Xiaowu

i TITLE OF INVENTION: Transposable Element Protein that Directs DNA

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

CURRENT APPLICATION NUMBER: US/09/232,446B

CURRENT FILING DATE: 1999-01-15

PRIOR PRILING DATE: 1998-01-15

PRIOR FILING DATE: 1998-01-15
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                    46.4%; Score 32; DB 4; Length 12; 66.7%; Pred. No. 47;
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                                                                                                                                                                                                                                                                                                   3; Indels
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66.7%; Pred. No. 4...
2; Mismatches
                                                                                                                                                                                                                                                                                                   0; Mismatches
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                          MOLECULE TYPE: peptide US-09-500-124-252
                                                                                                                                                                                                                                                                                                                                           2 KAMDPTPPL 10
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                                                                                                                                       TYPE: amino acid
TOPOLOGY: unknown
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1 LDPSPP 6
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LENGTH: 6
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; OTHER INFORMATION: Description of Unknown Virus Organism: Artificial US-09-739-852-7
                                                            Query Match
Best Local Similarity
                                                                                                                                    6 PTPPLW 11
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US-08-271-698-2
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                                                                                                                                                  NAME/KEY: misc feature; OTHER INFORMATION: Description of Artificial Sequence: phage display peptide US-09-315-926A-18
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, OTHER INFORMATION: Description of Unknown Virus Organism: Artificial
US-09-133-341-7
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APPLICANT: Hayward, Diane S.
APPLICANT: Ling, Paul D.
TITLE OF INVENTION:
FILE REFERENCE: 87512
CURRENT FAPLICATION NUMBER: US/09/133,341A
CURRENT PILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: WO 97US2243
EARLIER PILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hayward, Diane S.
APPLICANT: Hayward, Diane S.
APPLICANT: Ling, Paul D.
TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME FILE REPERBNCE: 97512
CURRENT APPLICATION NUMBER: US/09/739,852
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 3; Length 10;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                        42.0%; Score 29; DB 4; Length 12;
80.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 1; Indels
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US-09-133-341-7
; Sequence 7, Application US/09133341A
; Patent No. 6162440
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PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.68;
66.78;
                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
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ORGANISM: Unknown
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Patent No. 5358934

GENERAL INFORMATION:
APPLICANT: Barowsky, Dov
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: Of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: 5
STREET: 2421 N.W. 41st Street, Suite A-1
CORTY: Gainesville
Score 28; DB 4; Length 10;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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Patent No. 5439921;
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
PILING DATE: 19921211
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
  40.6%;
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80.0%;
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                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Search completed: May 26, 2005, 20:19:10
Job time : 41 secs
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 DPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-468-596-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08468596
; Sequence 2, Application US/08468596
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: of Peets
; TITLE OF INVENTION: of Peets
; NUMBER OF INVENTION: ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6;
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: SAILWANCHIK, DAVIG R.

REFERENCE/DOCKET NUMBER: UF/SES-127
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ ID NO: 2:

SEQUIENCE CHARACTERISTICS:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/468,596
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 1; 1 Pred. No. 4.1e+05;
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: FL
COUNTRY: USA
ZIP: 32606
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.1
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 DPTPP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: N
HYPOTHETICAL: N
HATI-SENSE: NO
US-08-271-698-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-596-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.1%; Score 27; DB 1; L
80.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 1;
PRIOR APPLICATION D478:
APPLICATION NUMBER: US 08/271,698
FILING DATE: 07-001-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY APRINT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPREMENS-POCKET NUMBER: 31,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TOWNER: UF/S&S-127
TELECOMMUNICATION TOWNER: UF/S&S-127
TELECOMMUNICATION TOWNER: SAGOO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

May 26, 2005, 20:27:26; Search time 38 Seconds (without alignments) 20.256 Million cell updates/sec

US-10-047-945-7

1 LKAMDPTP 8 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

909 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 8 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		major protein anti		alcohol dehydrogen		angiotensin-conver	transferrin - bovi		ICL2 protein - Par	enamelin f - bovin	leucokinin VII - M	Ca2+-transporting	tyrosine protein k	starvation-induced	ribosomal protein	proctolin - Americ	ribulose-bisphosph	proctolin - Atlant	halo-toxin - Pseud	bHLH transcription	244K exoantigen -	carboxylesterase (	DNA topoisomerase	globulin IV alpha	adipokinetic hormo	neuropeptide Led-C	adipokinetic hormo	adipokinetic hormo	adipokinetic hormo	hypertrehalosemic
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SU		B60274	IS1049	871919	S21288	PQ0008	A19780	PT0709	S71299	S10783	JS0317	I64832	I78890	S53508	S17255	HOROHA	PS0324	A60411	A61049	151317	A33098	809027	I48086	990608	A33995	B44960	A58620	855310	81059	80899
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df	Query Match	46.	41	41	39	30	3	30		30	ĕ	30.	27	2	27	27	2	27.	27	27	27	27	2	2	2	27	27	2	27	27
	Score	20	18	18	17	13	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
	Result No.	7	7	m	4	υ.	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

adipokinetic hormo endoglycosylcerami hynothetical prote	T-cell receptor be cellulase (EC 3.2. leucopyrokinin - M	sperm-activating p sperm-activating p sperm-activating p granulocyte-colony	D-mannonate nyarol cholecystokinin-5 20K protein - Rick Fc epsilon RIIb -	orf 3 rara 5'-regi mcrB protein - Esc
. B49823 B39745 S16324	PT0530 S21273 A23967	E60588 G60588 I54017	15//45 A32516 B31836 A46474	S15596 S55548
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227	227	20.72	2 2 2 2 2 2 2 2 2	25.0
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# ALIGNMENTS

```
major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
B;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: B60274
A;Accession: Breliminary
A;Accession: preliminary
A;Residues: 1-5 <NAG>
```

ö Gaps ö Query Match 46.5%; Score 20; DB 2; Length 5; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels

5 DPTP 8 1 DPAP 4 셤 ઠે

metallothionein-A - rainbow trout (fragment)
C;Species: Oncorbynchus mykiss (rainbow trout)
C;Species: Oncorbynchus mykiss (rainbow trout)
C;Species: Oncorbynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur. J. Blochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) me
A;Reference number: 151049
A;Accession: 151049
A;Accession: I51049
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accession: L4 <OLS>
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 41.9%; Score 18; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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Gaps

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4 MDP 6 중.. · 점

RESULT 3 871919 alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)

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transferrin - bovine (fragment)

(;Species: Bos prinigenius taurus (cattle)

(;Species: Bos prinigenius taurus (cattle)

(;Accession: A19780

R;Brock, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.

Biochen. Genet. 18, 851-860, 1980

A;Title: Electrophoretic mobility of N- and C-terminal monoferric fragments of bovine tally. R,Reference number: A19780; MUID: 81183891; PMID: 7225082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Fitler Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Faference number: PT0509; MUID:91277601; PMID:1711558
A.Faccession: PT0709
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Cispecies: Paramecium terraurelia
Cispecies: Paramecium terraurelia
Cispecies: Natura 1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
Ciscession: S71298
Eur. J. Biochem. 238, 121-128, 1996
A;Title: Characterization of centrin genes in Paramecium.
A;Reference number: S71298; MUID:96248429; PMID:8665928
A;Molecule type: protein
A;Residues: 1-7 <MAD>
A;Experimental source: strain 44-2
C;Genetics:
A;Genetic code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.2%; Score 13; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.2%; Score 13; DB 2; Lo
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-6 <FEE>
A,Experimental source: newborn thymus, strain BALB/c
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 2;
Pred. No. 2.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-6 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                              |::|
1 AVNP 4
         AMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
F;Accession: 52188 #13-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization A;Reference number: S21288; MUID:92272683; PMID:1590771
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-8 <MIL>
A;Molecule type: protein
A;Experimental source: var. Ulster Sceptre
C;Function: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin
      C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: 571919
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim. Biochys. Acta 1296, 41-46, 1996
A;Tsitle: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol de A;Reference number: 571919; MuID:96350418; PMID:8765227
A;Accession: 571919
A;Accession: 571919
A;Residues: 1-8 4TSU>
A;Residues: 1-8 4TSU>
A;Residues: 1-8 4TSU>
A;Roccession idellus
C;Keywords: NAD; oxidoreductase
C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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NyAlternate names: ficus latex peptide 1
(Species: Picus carica (common fig)
C)Species: Picus carica (common fig)
C)Bate: 07-Una-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C)Accession: PQ0008
R;Maruyama, S: Miyoshi, S: Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0008
A;Molecule type: protein
A;Respecimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor
|Species: Ctenopharyngodon idella (grass carp)
|Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
|Accession: S71919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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R;Chow, L.M.: Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein A;Reference number: IS8407; MUID:95060800; PMID:7970703
A;Accession: 178890
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Saccharomyces cerevisiae
A;Variety: strain 07173
C;Date: 23.Apr-1991 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: 817255
R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M. FEBS Lett. 284, 51-56, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
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C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                               tyrosine protein kinase - mouse (fragment)
C;Species: Was musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: 178890
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
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Best Local Similarity 100.0%;

Matches 2; Conservative 0
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Best Local Similarity 100.00
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A;Molecule type: protein
A;Residues: 1-4 <KOE>
C;Genetics:
A;Gene: SERCAlb
C;Keywords: hydrolase
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C;Species: Rattus norvegicus (Norway rat)
C;Accession: 164832
R;Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A;Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase is A;Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase is A;Reference number: 151892
A;Reference number: 151892
A;Reference number: Translated from GB/EMBL/DDBJ
A;Reference type: mRNA
A;Residues: 1-8 <-RES>
A;Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646
                                                                                                                                                               RESULT 9

$10783

enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C;Accession: $10783

R;Strawich, E.; Glimcher, M.J.

Bur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Teucokinin VII - Madeira cockroach

[c]Species: Leucophaea maderae (Madeira cockroach)

[c]Species: Leucophaea maderae (Madeira cockroach)

[c]Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

[c]Accession: JS0317

[R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

A;Hitle: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P19989
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
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Pred. No. 2.8e+05;
0; Mismatches 1;
  0; Mismatches
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A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
2; Conservative
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A;Residues: 1-8 <HOL>
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A, Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from A; Reference number: $17255, MUD: 91285106; PMID: 2060626
A; Accession: $17255
A; Robecule type: protein
A; Residues: 1-4 < GRO>
A; Cross-references: UNIPROT: P36515
C; Comment: A coding region for this protein could not be identified in the genome of Sac C; Genetics:
A; Genetics:
A; Genetics:
C; Reywords: mitochondrion; protein biosynthesis; ribosome
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A, Residues: 1-5 <STA>
A, Residues: 1-5 <STA>
A, Residues: 1-5 <STA>
A, Roce: 1-5 <STA>
A, Octos=-references: UNIPROT: P01373
A, Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac R, O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A, Title: Pentapeptide (proctolin) associated with an identified neuron.
A, Reference number: A94260; MUID: 8122865; PMID: 6113690
A, Contents: annotation; biological source
C, Comment: This peptide is found in the lateral white neurons, which occur (in the cockr innervate the striated hindgut muscles in insects and stimulate contraction of these mus C; Superfamily: proctolin
C; Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Periplaneta americana (American cockroach)
C.Species: Periplaneta americana (American cockroach)
C.Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C.Accession: A01644
R.Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A.Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects A.Reference number: A93048; MUID:76074708; PMID:576
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C.Species: Periplaneta american
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Query Match 27.9%; Score 12; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

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Search completed: May 26, 2005, 20:37:01 Job time: 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 20:19:15 ; Search time 172 Seconds (without alignments)
23.818 Million cell updates/sec

US-10-047-945-7 Title: Perfect score:

1 LKAMDPTP 8 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1612378 segs, 512079187 residues Searched:

790 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 8 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SILMMARIES

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# ALIGNMENTS

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MEDLINE-96350418; PubMed-8765227; DOI=10.1016/0167-4838 (96) 00051-9; Tsui H.T., Mock W.Y., Lau K.K., Fong W.P.; "Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol dehydrogenase."; Biochim. Biophys. Acta 1296:41-46(1996): Biochim. Biophys. Acta 1296:41-46(1996): GO: GO: GO: GO: GO: GO: GO: Fialcohol dehydrogenase activity; IEA.
                                                                                                                                                                                                                                                                                                                        Gutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

NCBI_TAXID=52617;

[1]

SEQUENCE FROM N.A.

He P., Xing J., Ren H.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY375240; AAQ83766.1; -.

NOM TER

SEQUENCE 8 AA, 882 MW; FA3DDEBAABA76AA6 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
Ctenopharyngodon idella (Grass carp).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Ctenopharyngodon.
NCBI_TaxID=7959;
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41.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Metallothionein B (Metallothionein A) (Fragment).
                                                                         8 AA.
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SEQUENCE.
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Best_Local Similarity
Matches 3; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A
            8
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                                                                                                                                                                                                                   NCBI_TaxID=12353;
                                                                                                                                                        Gp30.2 (Fragment)
                          2 ASTPSP
            AMDPTP
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                                                                                                                                                                      Name=30.2;
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                                                                                                          QBSBJ0;
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AC 09
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                                                                                                                                                                                                                                                                Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=235443;
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                                                             Gaps
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Bolwell G.P.;
"Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding."; Biochem. J. 283:813-821(1992).
PIR, S21288; S21288.
PIN, TER I I B B SEQÜENCE 8 AA; 771 MW; C37775A771B5BDDA CRC64;
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                                Query Match
41.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.5%; Score 17; DB 2; Length 8; Best Local Similarity 66.7%; Pred. No. 1.6e+06; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=H99;

STRAIN=H99;

Stuart L.T., Allen A., Dietrich F.S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY376718; AAQ88127.1; -.

GO; GO:0004506; F:squalene monooxygenase activity; IEA.

MONOOXygenase; Oxidoreductase.

NON TER

SEQUENCE 8 AA; 811 MW; 0467776AABIDD727 CRC64;
                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Squalene monooxygenase (EC 1.14.99.7) (Fragment)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
8
924 MW; DEA9D411B1B76AB5 CRC64;
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                                                                                                                                                                                                                                                     Cryptococcus neoformans var. grubii H99.
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Solanum tuberosum (Potato)
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Matches 3; Conserva
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8 AA;
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2 DPT 4
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NON TER
SEQUENCE
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Q6U7R2
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                                                                                                                                           Bacteriophage RB69.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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Pred. No. 1.6e+06;
0; Mismatches 1; Indels
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Kolesinskiene G., Nivinskas R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ458400; CAD30256.1; -.
NON_TER 8
                                                                                                                                                                                                                                                                                                  Nivinskas R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AJ439452; CAD28423.1; -.
NON TER 8
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
010-02 protein (Fragment).
                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
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  PRT;
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PRELIMINARY;
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collision.

-!- SUBCELDULAR LOCATION: Secreted.
-!- SUBCELDULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: First appears in the ovarian follicles furing vitellogenesis. Accumulates in the occytes before being secreted during fertilization. Expression continues in the embedded occyte. Accumulates in the egg capsule after fertilization.
-!- MASS SPECTROMETRY: NM-596.6; METHOD=NALDI; RANGE=1-6; NOTE=Ref.1. Amidation; Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
"Isolation, identification and synthesis of locustamyotropin II, an additional neuropeptide of Locusta migratoria. Member of the cephalomyotropic peptide family.";
Insect Biochem. 20:479-484(1990).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                               TISSUE=Egg;
MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide.";
Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-1- FUNCTION: Attracts sperm increasing the chances of gamete
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Sperm attracting peptide SepSAP.
Sepia officinalis (Common cuttlefish).
Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
                                                                                                                                                            SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Locustamyotropin 2 (LOM-MT-2).
Locusta migratoria (Migratory locust).
Locusta migratoria (Migratory locust).
Reptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Orthoptera; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
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PROSITE; PS00539; PYROKININ; 1.
Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.6%; Score 14; DB 1; Length 6; Best Local Similarity 66.7%; Pred. No. 1.6e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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6 AA; 597 MW; 72C8676AA0470000 CRC64;
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-!- SIMILARITY: Belongs to the pyrokinin family.
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75.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 1;
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Best Local Similarity
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SEQUENCE
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LMT2 LOCMI
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                  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                         TISSUE=Epidermis;
MEDLINE=97165493; PubMed=9013254;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
Identification and mRNA developmental profiles of two ultraspiracle isoforms in the epidermis and wings of Manduca sexta.";
Insect Mol. Biol. 6:41-53(1997).
EMBL; US7921; ARB64235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 15; DB 2; Length 8; 50.0%; Pred. No. 1.6e+06; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miaw S.-C., Ho I.-C.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Repressor of GATA (Fragment).
                                                                                                                                                                                                                                                                                                                                                          8 AA; 892 MW; F165BB0415A76B16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 943 MW; FE3411B771B6C766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 2; Dred. No. 1.6e+06; O; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 172:170-177(2004)
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60.0%;
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NON TER 8
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Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0
nes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57B6;
PubMed=14688323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MDPTP 8
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1 MEPS 4
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Q99P40;
01-JUN-2001 (
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ID SAPP_SEPOF
AC P83569;
DT 29-MAR-2004
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RESULT 8

099P40

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               americana.";
Regul. Pept. 71:199-205(1997).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mair J., Rouse D.A., Morris S.L.;
"Nucleotide sequence analysis of the ribosomal S12 gene of
Mycobacterium intracellulare.";
Mycobacterium intracellulare.";
Mycobacterium intracellulare.";
"Nucleot Acids Res. 21:1039-1039139.
-I- FUNCTION: One of the primary rRNA binding proteins, it binds
directly to 16S rRNA where it nucleates assembly of the head
domain of the 30S subunit. Is located at the subunit interface
close to the decoding center, probably blocks exit of the B-site
tRNA (By similarity).
-I- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
and S11 (By similarity).
-I- SIMILARITY: Belongs to the ribosomal protein S7P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
TISSUB=Corpora cardiaca;
MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=907.92; METHOD=Electrospray; RANGE=1-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-3 (Pea-K-3).
Periplaneta americana (American cockroach).
Bukaryyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Nooptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium intracellulare.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14; DB 1; Length 8;
Pred. No. 1.6e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE=Ref.1.
--- SIMILARITY: Belongs to the kinin family.
Amidation; Direct protein sequencing; Neuropeptide.
MOD_RES 8 Glycine amide.
SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
30S ribosomal protein S7 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.6%;
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                             STANDARD;
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P33564;
                                                                                                                                                                             PK3 PERAM
P82687;
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RS7_MYCIT
                                                                                                   RESULT 111
PR3 PERAM
PR3 PERAM
DD OS-JU
DDT OS-JU
DD OS-J
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TISSUE=Bone marrow;

MEDLINE=95002916; PubMed=7919324;

Tighe J.E., Calabi F.;

Tighe J.E., Calabi F.;

"Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                     EMBL; L08171; AAA25376.1; -.
PIR; S35538; S35538.
HAWAP; MF_00480; -; 1.
InterPro; IPR000235; Ribosomal_S7.
PROSITE; PS0052; RIBOSOMAL_S7; PARTIAL.
Ribosomal protein; RNA-binding; rRNA-binding.
INIT MET 0 By similarity.
NON_TER 8
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase beta subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood 84:2115-2121(1994).
BmBL; 874094; AAD14973.2; -.
NON TER
SEQÜENCE 8 AA; 929 MW; 30B764405B17244B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14; DB 2; 1
Pred. No. 1.6e+06;
2; Mismatches 0
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Name=runt/68nt/MTGB;
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50.0%;
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Brassica napus (Rape).
Chloroplast.
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O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                 Zhang Z.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF264734; AAF74768.1; -. GO; GO:0009507; C:chloroplast; IEA.
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Heslewood M., Quinn C.J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184659; AAF03860.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
AtpB (Fragment).
                                                                                                                                                                                                                                                                                                                                                         8 8 AA; 919 MW; ECAlBIB764404406 CRC64;
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Search completed: May 26, 2005, 20:36:15 Job time : 176 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2005, 20:18:30 ; Search time 157 Seconds (without alignments) 19.708 Million cell updates/sec Run on:

US-10-047-945-7 Perfect score: Title:

1 LKAMDPTP 8 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

160390 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 8 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2003as:*geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

tion	8 Synthetic							9 Coxsackie	2 N-termina	5 Hepatitis	5 Partial s	8 Human VPL	2 Vesicular	6 Synthetic			7 SH3 antag	3 SH3 antag	2 SH3 antag	Scaf	H11	5 H11 bindi	8 H11 bindi	0 H11 bindi	0 Src homol
Description	Abb80228	Aaw53842	Abb80224	Aaw45995	Adk10228	Aar37031	Aab68473	Aay50089	Abr82052	Adk01475	Aab74035	Abb81338	Aaw24922	Aab74036	Abb81339	Aay40821	Aab1724	Aab1723	Aab17232	Aab30156	Aam46490	Aam4649	Aam45098	Aam44790	Abb7324
ID	ABB80228	AAW53842	ABB80224	AAW45995	ADK10228	AAR37031	AAB68473	AAY50089	ABR82052	ADK01475	AAB74035	ABB81338	AAW24922	AAB74036	ABB81339	AAY40821	AAB17247	AAB17233	AAB17232	AAB30156	AAM46490	AAM46495	AAM45098	AAM44790	ABB73240
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% Query Match	100.0	55.8	55.8	55.8	55.8	53.5	53.5	53.5	51.2	51.2	48.8	48.8	48.8		48.8	48.8	48.8	48.8	48.8	48.8		48.8	48.8	48.8	48.8
Score	43	24	24	24	24	. 23	23	23	22	22	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
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Abb73226 Src homol	Abb73225 Src homol	Adc44630 Endotheli	Adj73394 SH3 antag		Adj73380 SH3 antag	E	E	EH	E	Adj51975 CH1 delet	E		IgG	IgG		IgG	Adq07268 IgG purif		Abp20550 HIV A03 m
7 5 ABB73226	7 5 ABB73225	7 7 ADC44630	7 7 ADJ73394	7 7 ADJ73379	7 7 ADJ73380	7 8 ADJ53013	7 8 ADJ53014	7 8 ADJ53028	7 8 ADJ51974	7 8 ADJ51975	7 8 ADJ51989	7 8 ADQ08405	7 8 ADQ08528	7 8 ADQ28430	7 8 ADQ28553	7 8 ADQ07145	7 8 ADQ07268	8 4 ABP12619	8 4 ABP20550
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

ABB80228 standard; peptide; 8 AA.

ABB80228;

06-NOV-2003 (first entry)

Synthetic LINF, LT-8.

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. 

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

e.g. Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

Sequence 5 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 8; Conservative
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hödgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins from requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                    Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                        SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
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Length 5;
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DB 2; Le
. 1.8e+06;
Score 24; DB 2; Pred. No. 1.8e 0; Mismatches
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 55.8%,
100.0%; Pre-
0; '
                                                                                                                                                                                              ABB80224 standard; peptide; 5 AA.
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55.8%;
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                                    Conservative
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tes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Query Match
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reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                       New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a novel polypeptide encoded by an alternative
                                pathogenic virus; alternative reading frame; antigenic determinant;
virucide; vaccine; therapeutic agent; infection; HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-anomer; beta-glycosylamine linked glycoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        component #1 of N-linked glycoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24; DB 8; I
Pred. No. 1.8e+06;
1; Mismatches 1;
     Human papillomavirus peptide #2283.
                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 198; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR37031 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                    Habel
                                                                                                                                                      24-JUL-2003; 2003WO-EP008112.
                                                                                                                                                                                24-JUL-2002; 2002AT-00001124.
11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                    Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                        Human papillomavirus
                                                                                                                                                                                                                         (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                               WPI; 2004-169243/16.
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                                                                                                  WO2004011650-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1991;
11-AUG-1992;
                                                                                                                             05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
28-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP538230-A1
                                                                                                                                                                                                                                                    Mattner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR37031;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR37031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non-naturally occurring peptide(s) - which are based on portions of somatostatin, somatostatin receptors and insulin-like growth factor binding protein.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                               Hormone, receptor, antibody, vaccine, immunogen, somatostatin, IGF, insulin-like growth factor binding protein, ILGFBP, SSTR, diabetes, somatostatin receptor, insulin-like growth factor.
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 55.8%; Score 24; DB 7; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%; Score 24; DB 2; Length 8; 66.7%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                    Peptide #17 based on human SSTR 2 (residues 282-290).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kingston DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Page 9; 136pp; English
                                                                                                                                                     AAW45995 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK10228 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-AU000312
                                                                                                                                                                                                                                                                                                                                                                                                                                                96AU-00009990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Westbrook SL,
                                                                                                                                                                                                           (first entry)
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                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-018427/02.
Query Match
Best Local Similarity
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                                                        1 LKAMD 5
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AISPTP (
                                                                                  LKAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                               WO9744352-A1
                                                                                                                                                                                                           03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerraty NL,
                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1997
                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                AAW45995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK10228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                             Matches
                                                                                                                                       RESULT 5
ADK10228
ID ADK1
XX
AC ADK1
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DT 06-M
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Gaps

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1; Indels Length 8;

Gaps

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us-10-047-945-7.closed.rag

Dwek RA, (MONS )

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The present sequence represents a mutated portion of an integrase. The specification describes a method for targeting integration of retrotransposon of Tyl-copia group to desired location on a chromosome. The method uses a modified integrase in a retrotransposon, where the modified integrase contains a coding sequence for a peptide portion which specifically binds to protein bound to the chromosome or to particular nucleic acid sequences on chromosome. The method is useful for targeting integration of a retrotransposon of the Tyl-copia group to a desired chromatin targeting of Ty5 is useful for tagging genes which are affected by aging and for studying oncogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epitope. The invention relates to a novel method for designing degenerate PCR primers (AAZ30975-Z31000, AAZ32601- AAZ32611) for amplifying target polynucleotides. This method comprises identifying uniquely conserved amino acid sequences (e.g, this epitope) in target proteins; synthesising degenerate polynucleotides encoding the conserved sequences; and substituting the synthesised polynucleotides with up to four predetermined nucleotides (e.g., inosine) at degenerate nucleotide positions. The nucleic acids comprise no more than 7 degenerate positions, have no more than 2 adjacent predetermined nucleotides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a conserved Coxsackievirus A (serotype A16) VP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virus; epitope; target; degenerate; PCR; primer; amplification; VP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein 2A, conserved, base analogue, inosine, predetermined nucleotide, diagnosis, enterovirus, poliovirus
                                                                                                                                                                                                                                                                                                                              Score 23; DB 4; Length 6;
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Designing degenerate polymerase chain reaction primers.
                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coxsackievirus A VP1 conserved epitope 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 18; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY50089 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                         53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US007513
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                                                                                                                                                                                                                                                                                                                                                                          3; Conservative
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N-PSDB; AAZ32608.
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         4 MDPTP 8
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LDPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kilpatrick DR;
                                                                                                                                                                                                                                                                                    Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9953097-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50089;
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           886666666666888
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                                                                                                                                                                                                                                                                                                                         A peptide of 5-25 amino acid residues (pref. one of the pentapeptides AAR37031-3 or an atriopeptin e.g. atriopeptin A or D, see AAR37337-8) having an activated carboxyl group capable of forming a betaglycosylamine linked glycoconjugate is reacted with an unprotected betaglycosylamine deriv. of an oligosaccharide. The deriv. is prepared by reacting an unprotected oligosaccharide the deriv. is prepared by with saturated ammonium bicarbonate at pH 80-8.5. The N-linked glycoconjugate is produced under conditions to directly maintain the beta-anomeric configuration. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeting integration of retrotransposon or retrovirus into silent chromatin by transforming a cell with modified integrase having a coding sequence for a peptide portion that interacts with chromatin at desired
                                                                                                                                                                                      N-linked peptide glyco-conjugate(s) prepn. - by reacting oligosaccharide(s) with ammonium bi:carbonate to maintain beta-anomeric configuration, and avoid sepn. of anomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin; chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
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1.8e+06;
                                                                                                    Wong SYC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.5%; Score 23; DB 100.0%; Pred. No. 1.8 ive 0; Mismatches
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                                                                                                  Manger ID, Rademacher TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB68473 standard; peptide; 6 AA.
                                                     OXFORD GLYCOSYSTEMS LTD.
                                                                                                                                                                                                                                                                                 Claim 3; Page 32; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Col 66; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces paradoxus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-342676/36.
                                                                                                                                            WPI; 1993-128045/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                   MONSANTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5 AA;
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15-JAN-1999; 15-JAN-1998;

Voytas DF,

US6228647-B1

08-MAY-2001

23-JUL-2001

AAB68473;

RESULT 7 AAB68473

Matches

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predetermined nucleotides are 3 bases away from the 3' end of the synthesised strand. The degenerate primers are useful for amplifying target polynucleotides by the polywerses chain reaction (PCR). The use of the method of designing degenerate primers useful for the detection of polioviruses in clinical samples is described in USS85477. The degenerate primers facilitate PCR amplification of unknown polynucleotides, where the amino acid sequence encoded is known. The primers also allow for the subsequent molecular based diagnosis with a serologically derived diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method of screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase. The method comprises: (1) exposing a candidate compound to an oligosaccharide and a polypeptide comprising a beta subunit of AMP kinase, or its mutant and/or fragment that binds an oligosaccharide; and C12 assessing the ability of the candidate compound to modulate binding of the polypeptide to the oligosaccharide. An AMP kinase beta subunit oligosaccharide binding domain sequence has antidiabbetic, cytostatic, antiarteriosclerotic and anorectic activities, and can be used in gene therapy. The method is useful for screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase for treating or preventing a condition associated with AMP kinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for a compound that modulates the binding of an oligosaccharide to a beta subunit of AMP kinase by assessing the ability of the candidate compound to modulate binding of the polypeptide to the oligosaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g., diabetes, atherosclerosis, obesity or cancer. The present sequence represents an N-terminal sequence from AMPK beta 1 (68-163) fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMP kinase beta subunit oligosaccharide binding domain, AMP kinase, oligosaccharide binding domain; enzyme; antidiabetic; gene therapy; antiarteriosclerotic; anorectic; cytostatic; diabetes; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal sequence from AMPK beta 1 (68-163) fusion protein SEQ ID:31.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                              Score 23; DB 2; Length 7;
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR82052 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                          53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2002; 2002WO-AU001769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-2001; 2001AU-00009728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                      4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-559281/52.
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                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                             2 KAMDPTP
                                                                                                                                                                                                                                                                                                                                                               KXTDPPP
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                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR82052;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel polypeptide encoded by an alternative
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                           pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection.
protein, which is used in an example from the present invention
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                                                                                            0; Indels
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Pred. No. 1.8e+06;
3; Mismatches 2; Indels
                                                             DB 6; Le
1.8e+06;
                                                           51.2%; Score 22; DB 100.0%; Pred. No. 1.8 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 127; 220pp; English.
                                                                                                                                                                                                                                                                                                                              Hepatitis C virus 1b peptide SeqID127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB74035 standard; peptide; 4 AA.
                                                                                                                                                                                                                                  ADK01475 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Habel A;
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37.5%;
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11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                             06-MAY-2004 (first entry)
                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.5
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mattner F, Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTE-) INTERCELL AG.
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                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus
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                              Sequence 7 AA;
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                                                                                                                          3 AMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2004.
                                                                                                                                                                                                                                                                  ADK01475;
                                                           Query Match
                                                                             Best Loc
Matches
                                                                                                                                                                                                      RESULT 10
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ID AAB7
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AAB74035;

Synthetic.

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The present invention describes an antibody which specifically recognises the human VPLF (vascular endothelial growth factor (VBGF)/plateletactive derived growth factor (PBGF)/plateletactive of this protein as growth factor. The antibody has vasotropic, vulnerary, nephrotropic, cardiant, antidiabetic, antiarteriosclerotic, antianaemic, osteopathic, anticheumatic, antiarthritic and antipsoriatic activities. The antibody is applicable in diagnostics and remedias for VPLF-participated diseases like arthritis, ischaemic diseases and retarded wound healing. The present sequence represents a human VPLF related peptide sequence, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Etiological agent; autoimmune disease; systemic lupus erythematosus; SLE; Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
                                                                                                                                                                                                                          Antibody specifically recognizing VPLF or its variant and inhibiting its activity, applicable in diagnostics and remedies for VPLF-participating diseases like arthritis, ischemic diseases and retarded wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of immunogenic agent in auto-immune disease - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
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Pred. No. 1.8e+06;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                Example; Page 59; 136pp; Japanese
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19-OCT-2001; 2001WO-JP009218.
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75.0%;
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                                          19-OCT-2000; 2000JP-00319985.
                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK. (HELI-) HELIX RES INST.
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91US-00648205
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                                                                                                                                               Furuya A;
                                                                                                                                                                                        WPI; 2002-394558/42.
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wes 3; Conserv
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31-JAN-1991;
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17-OCT-1997
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                                                                                                                                               Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence sequence is provided in a specification relating to a novel vascular endothelial growth factor (VBGF)/platelet derived growth factor (VBGF)/platelet derived growth factor (PBGF)-like factor of 345 amino acids, or to a sequence in which at least one amino acid is deleted, replaced or added compared to the native sequence. The nucleotide sequence encoding the VBGF/PDGF-like factor may be integrated into a vector and used to transform a host cell. The VBGF/PDGF-like factor may be used in the development of agents for transform of a section treating diseases associated with abnormal neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; VPLF; VEGF/PDGF-like factor; vascular endothelial growth factor; platelet-derived growth factor; antibody; inhibition; growth factor; vasctropic; variation ential antidatetic; antianaemic; antidateticsclerotic; osteopathic; antirheumatic; antianthritic; antipsoriatic; arthritis; ischaemic disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New VEGF/PDGF-like factor useful for the development of treating agents for diseases accompanied by accentuation of abnormal neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      Partial sequence contained in commercially available plasmid pMbac.
                                                                                                                                           VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF; platelet derived growth factor; PDGF; neovascularisation; disease.
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VPLF related peptide sequence SEQ ID NO:34.
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(HERI-) HERIKKUSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%;
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                                                              (first entry)
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                09-AUG-2001
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Synthetic.

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ABB81338;

RESULT 12 ABB81338

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Gaps

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Sequence 6 AA;

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The invention relates to methods to determine the etiological agent of autoimmune diseases such as systemic lupus erythematosus (SLB). A common antigen for SLE and closely related disorders is the 60 kD protein-RNA particle: Ro/SSA, present in all cells studied to date. Staphylococcus VB protease digestion of this protein reveals bands of 51, 40, 35, 28 and 13 kD which are strongly immunoreactive with SLE autoantibodies. From the 13 kD band, peptide AAWA-911 demonstrated maximal antigenicity against anti-Ro/SSA autoantibodies beptides immunoreactive with SLE autoantibodies can then be used to screen for other peptides reactive with the antibodies. An example of such a peptide is the sequence presented here which is derived from the nucleocapsid protein of the Indiana serotype of the vesicular stomatitis virus. (Updated on 25-MAR-2003 to correct PP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence sequence is provided in a specification relating to a novel vascular endothelial growth factor (VEGP)/platelet derived growth factor (PDGP)-like factor of 34s amino acids, or to a sequence in which at least one amino acid is deleted, replaced or added compared to the native sequence. The nucleotide sequence encoding the VEGF/PDGF-like factor may be integrated into a vector and used to transform a host cell. The VEGF/PDGF-like factor may be used in the development of agents for treating diseases associated with abnormal neovascularisation. The present sequence is the N-terminal sequence of the protein shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New VEGF/PDGF-like factor useful for the development of treating agents for diseases accompanied by accentuation of abnormal neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
identifying protein sequences homologous to self-antigen sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF; platelet derived growth factor; PDGF; neovascularisation; disease.
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                                                                                                                                                                                                                                                                                                                                                                                              48.8%; Score 21; DB 2; Length 5; 80.0%; Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                    Example 2; Col 17; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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Matches 4; Conserv
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LKALD 5
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                                                                                                                                                                                                                                                                                                                                    platelet-derived growth factor; antibody; inhibition; growth factor; vasotropic; valnerary; nephrotropic; cardiant; antidiabetic; antianaemic; antiarteriosclerotic; osteopathic; antirheumatic; antiarthritic; antipsoriatic; arthritis; ischemic disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody specifically recognizing VPLF or its variant and inhibiting its activity, applicable in diagnostics and remedies for VPLF-participating diseases like arthritis, ischemic diseases and retarded wound healing.
                                                                                                                                                                                                                                                                                                                      Human; VPLF; VEGF/PDGF-like factor; vascular endothelial growth factor;
                                                 Gaps
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                Score 21; DB 4; Length 6;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     Human VPLF related peptide sequence SEQ ID NO:35.
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                                                                                                                                                                                            ABB81339 standard; peptide; 6 AA.
                48.8%;
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                                                 Conservative
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Query Match
Best Local Similarity
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nes 3; Conserv
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Search completed: May 26, 2005, 20:33:20 Job time : 164 secs

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May 26, 2005, 20:36:28 ; Search time 133 Seconds (without alignments) 20.750 Million cell updates/sec
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Appl	Appl	Appl										Appl
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	Description	Sequence 7,	Sequence 3	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 26,
KIES		US-10-047-945-7	US-10-047-945-3	JS-09-758-128-20	JS-09-758-128-23	JS-09-758-128-26	8-128-29	8-426-20	US-09-758-426-23	8-426-26	8-426-29	JS-09-758-198-20	8-198-23	JS-09-758-198-26
SUMMAKIES	Ω	US-10-0	US-10-0	S-09-75	S-09-75	S-09-75	S-09-75	8-09-75	S-09-75	S-09-75	S-09-75	S-09-75	JS-09-758-198-2	S-09-75
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Corresponds to fragment 1-8 of 2 above.

LOCATION: COTHER INFORMATION: Synthetic. US-10-047-945-7

NAME/KEY:

Length 8; Indels

Query Match 100.0%; Score 43; DB 14; Best Local Similarity 100.0%; Pred. No. 1.3e+06; Matches 8; Conservative 0; Mismatches 0;

1 LKAMDPTP

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APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE REFERENCE: 104786/0214
CURRENT APPLICATION NUMBER: 09/09/758,128
CURRENT FILING DATE: 1990-02-05
PRIOR FILING DATE: 1990-02-05
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PALENTIN VEr. 2.0
SEQ ID NO 23
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Patent No. US20020107187A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187A1man L.
APPLICANT: MESTEROCK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Sequence 26, Application US/09758128

Patent No. US20020107187A1

SEGURATION:
APPLICANT: KINGSTON, David J.
APPLICANT: WESTERCOK, Simon L.
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT APPLICATION NUMBER: 09/194,218

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 26

SEG ID NO 26
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Pred. No. 1.3e+06;
1; Mismatches 1;
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Pred. No. 1.3e+06;
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Best Local Similarity
Matches 4; Conserv
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  GENERAL INFORMATION:
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US-09-758-128-29
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Sequence 20, Application US/09758128

Patent No. US20020107187A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY, No. US20020107187A1man L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODIFIEDS, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT APPLICATION NUMBER: 09/194,218

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATENTI VET. 1995-05-05

SEQ ID NO 20

LENGTH: 8
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          Sequence 3, Application US/10047945
Publication No. US20030157555A1
SEQUENCE INFORMATION:
GENERAL LIPPS, BIRE V.
APPLICANT: LIPPS, BREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (198) IMPLICATED DISORDERS
FILE REPERENCE: FWLPA7015US
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR FILING DATE:
PRIOR FILING DATE:
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Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.3e+06;
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SOFWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 3
LENGTH: 5
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; Sequence 23, Application US/09758128
; Patent No. US20020107187A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 4; Conservative
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US-09-758-128-20
US-10-047-945-3
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NAME/KEY:
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SERRATY INFORMATION:

APPLICANT: WESTBROOK, Simon L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODILATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: WOBERLOGGE 2017 Set 2017 Se
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Patent No. US20020169116A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: KINGSTON, David J.
APPLICANT: WESTBROOK, Simon L.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF FILE REFERENCE: 0.6796/0.14
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF PILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT PILING DATE: 2001-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 29
LENGTH: 8
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PRIOR APPLICATION NUMBER: 09/194,218
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Best Local Similarity 66.7°
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Best Local Similarity 66.7
Matches 4; Conservative
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1 AISPTP 6
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; ORGANISM: Bovine
US-09-758-426-20
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; ORGANISM: Rat
US-09-758-128-29
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US-09-758-426-23
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Sequence 26, Application US/09758426

| Patent No. US30020169116A1
| GRUERAL INFORMATION:
| APPLICANT: KINGSTON, David J.
| APPLICANT: GERRATY, No. US20020169116A1man L.
| APPLICANT: GERRATY, No. US20020169116A1man L.
| APPLICANT: GERRATY, No. US20020169116A1man L.
| TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;
| TITLE OF INVENTION: — PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF;
| TITLE OF INVENTION: — PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF;
| CURRENT APPLICATION NUMBER: US/09/758,426
| CURRENT FILING DATE: 2001-01-12
| PRIOR PEPLICATION NUMBER: 09/194,218
| PRIOR PELICATION NUMBER: 09/194,218
| PRIOR FILING DATE: 1996-02-05
| PRIOR FILING DATE: 1996-02-05
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: PATENTIN VEY: 2.0
| SEQ ID NO 26
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Patent No. US20020169116A1

GENERAL INFORMATION:
APPLICANT: KINOSTON, David J.
APPLICANT: GENERATY, No. US20020169116Alman L.
TITLE OF INVENTION: WODULANING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: PERTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/194,218
FRIOR FILING DATE: 1999-02-05
FRIOR FILING DATE: 1999-02-05
FRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENT OF THE US OF THE
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Pred. No. 1.3e+06;
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PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN'
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver: 2.0
LENGTH: 8
LENGTH: 8
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Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Porcine
US-09-758-426-23
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1 AISPTP
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ORGANISM: Mouse
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LENGTH: 8
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Publication No. US20020187925A1

Publication No. US20020187925A1

GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020187925A1man L.
APPLICANT: WESTRROWS: Simon L.
APPLICANT: WESTRROWS: Simon L.
APPLICANT: WESTRROWS: Simon L.
APPLICANT: WESTRROWS: O16786/0214

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REPREBENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,198

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SEQ ID NO S: 58

LENGTH: 8

LENGTH: 8
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Publication No. US20020187925A1

Publication No. US20020187925A1

Publication No. US20020187925A1

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY No. US20020187925A1man L.

APPLICANT: GERRATY

NO. US20020187925A1man L.

APPLICANT: GERRATY

FILE REPERROKE: 016786/0214

CURRENT APPLICATION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REPERBENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,198

CURRENT PILING DATE: 2001-01-12

FRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR PELING DATE: EARLIER FILING DATE: 1999-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ 1D NOS: 58

SEQ 1D NO 23
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                                                                                                                                        Score 24; DB 9; Length 8; Pred. No. 1.3e+06; 1; Mismatches 1; Indels
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Pred. No. 1.3e+06;
1; Mismatches 1; Indels
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                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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1 AISPTP 6
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1 AISPTP 6
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ORGANISM: Bovine
                                            ; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-29
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US-09-758-198-20
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SEQ ID NO 29
                        LENGTH: 8
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Sequence 29, Application US/09758198

Sequence 29, Application US/09758198

Publication No. US20020187925A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

APPLICANT: MESTBROOK, Simon L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-02

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 1996-05-22

PRIOR PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SEGURANT SEQ ID NOS: 58

LENGTH: 8

LENGTH: 8

LENGTH: 8
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Publication No. US20020187925A1
Fublication No. US20020187925A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: WESTBROOK, Sinon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS;
TITLE OF INVENTION: WODULATION SAMINES: US/09/788,198;
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218;
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: PCT/AU97/00312;
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: PCT/AU97/00312;
PRIOR APPLICATION NUMBER: EARLIER PLILING DATE: 1997-05-22;
PRIOR APPLICATION NUMBER: EARLIER PLILING DATE: 1996-05-22;
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22
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                                                                                                                                                            Indels
                                                                                                         Length 8;
                                                                                                         Score 24; DB 9; I
Pred. No. 1.3e+06;
1; Mismatches 1;
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Best Local Similarity 66.7-
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Best Local Similarity 66.7
Matches 4; Conservative
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TYPE: PRT
CRGANISM: Porcine
US-09-758-198-23
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US-09-861-661-20
i Sequence 20, Application US/09861661
i Publication No. US20030045676A1
i GENERAL INFORMATION:
i APPLICANT: KINGSTON, DAVID J.
i APPLICANT: KINGSTON, DAVID J.
i APPLICANT: WESTERCOK, SIMON L.
i TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
i FILE REFERENCE: 042-70/0135
i CURRENT FILING DATE: 2001-05-22
i PRIOR APPLICATION NUMBER: US/194,218
i PRIOR FILING DATE: 1999-02-05
i PRIOR FILING DATE: 1999-02-05
i PRIOR FILING DATE: 1996-05-22
i NUMBER: OF SEQ ID NOS: 59
i SOPTWARE: PATENTIN Ver. 2.1
i SEQ ID NO 20
i LENGTH: B
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Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                     1; Indels
                                                                            55.8%; Score 24; DB 9; Length 8; 66.7%; Pred. No. 1.3e+06; ive 1; Mismatches 1; Indels
                                                                          Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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1 AISPTP 6
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1 AISPTP 6
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; ORGANISM: BOB SP.
US-09-861-661-20
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-29
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Search completed: May 26, 2005, 20:49:24 Job time : 157 secs

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Sequence 3, Application US/08657163A
Patent No. 574449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND TITLE OF INVENTION: SYNTHETIC LINES AND THEIR TITLE OF INVENTION: UTILITY AS TREATMENT FOR BNVENOMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT; BINIE V. LIPPS AND FREDERICK W. LII
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AN
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR INVEMER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MINOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
RIGHT OF APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 25 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTONEY ARBENT HORDATION: DATA:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,1919
REGISTRATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: ALL STRUCTS STRUCTS STRUCTS TOPOLOGY: LINEAR MOLECULE TYPE: PEPTIDE IN SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-08-657-163A-3
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58, Appl
58, Appl
68, Appl
68, Appl
39, Appl
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                                                                                                                                     May 26, 2005, 20:30:57; Search time 40 Seconds (without alignments) 14.930 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
Sequence 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5G_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-428-082B-288
US-09-428-082B-289
US-09-428-082B-303
US-077-789-184-190
US-08-475-263-190
US-08-477-36-190
US-08-477-34-190
US-08-477-34-190
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US-07-926-786-1

US-09-147-943-35

US-09-147-943-35

US-08-666-473-60

US-07-657-769B-1

US-07-657-769B-21

US-07-657-769B-21

US-07-657-769B-21

US-07-789-184-68

US-08-475-263-68

US-08-477-362-68

US-08-477-39-08

US-08-66-473-39

US-09-428-082B-288

US-09-428-082B-288

US-09-428-082B-288

US-09-428-082B-288

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US-09-428-082B-288

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US-09-428-082B-288
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Maximum Match 100%
Listing first 45 summaries
                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                         US-10-047-945-7
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Match Length
                                                                                                                                                                                                                                                                                          1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                     Perfect score:
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Maximum DB
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	ALIGNMENTS					
_	US-08-485-886-72	-	ß	20 46.5	45	
	US-08-485-886-70	Н	ī,	46.	44	
	US-08-398-028B-46	Н	Ŋ	46.	43	
72,	US-08-475-263-72	н	2	46.	42	
70,	US-08-475-263-70	Н	Ŋ	46.	41	
Sequence 46, Appl	US-08-460-343B-46	Н	Ŋ		40	
72,	US-07-789-184-72	-	S		39	
70,	US-07-789-184-70	Н	Ŋ	20 46.5	38	
1, 2	US-08-468-596-1	-	ū	20 46.5	37	
ų	US-08-271-698-1	Н	Ŋ	46.	36	
٦,	US-07-989-290-1	-	ß	20 46.5	35	
99	US-07-657-769B-66	-	2		34	
64,	US-07-657-769B-64	-	Ŋ	20 46.5	33	
Sequence 27, Appl	US-07-657-769B-27	-	ស		32	
25,	US-07-657-769B-25	-1	2		31	
Sequence 190, App	US-08-018-760-190	m	œ		30	
•	US-08-485-695-190	m	80	48.	53	
	US-08-473-489A-190	m	œ		28	

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GENERAL INFORMATION:

APPLICANT: VOYLES, Daniel F.

APPLICANT: Gai, Xiaowu

TITLE OF INVENTION: Transposable Element Protein that Directs DNA

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

TITLE OF INVENTION: Integration to Specific Chromosomal Sites

FILE REFERENCE: 2-98

CURRENT APPLICATION NUMBER: US/09/232,446B

CURRENT APPLICATION NUMBER: US 60/071,383

PRIOR APPLICATION NUMBER: US 60/071,383

PRIOR APPLICATION NUMBER: US 60/071,383

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 24

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: mxutant peptide; OTHER INFORMATION: sequence US-09-232-446B-24
                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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1 LDPSP 9
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US-09-147-933-35
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rademcher, Thomas W.
APPLICANT: Rademcher, Tan D.
APPLICANT: Wong, Simon
APPLICANT: Wong, Simon
APPLICANT: Dwek, Raymond A.
TITLE OF INVENTION: Method for Producing Synthetic N-Linked
TITLE OF INVENTION: Glycoconjugates
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.5%; Score 23; DB 1; Length 5; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                          0; Indels
                                                                     Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/07/926,786
FILING DATE: 19920811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ουνκΕSSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
                                                                55.8%; Score 24; DB 1; L. 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/776911
FILING DATE: 15-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/394691
FILING DATE: 16-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-232-446B-24
; Sequence 24, Application US/09232446B
                                                                                                                                                                                                                                                              RESULT 2
US-07-926-786-1
'Sequence 1, Application US/07926786
'Patent No. 5280113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
; ORIGINAL SOURCE: SYNTHETIC US-08-657-163A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (314)694 - 3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (314) 694-5435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                Query Match 55.8
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19:
CLASSIFICATION:
                                                                                                                                                                                         1 LKAMD 5
                                                                                                                                                       1 LKAMD 5
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Length 6;

Score 23; DB 3; Pred. No. 4.1e+05;

53.5%;

2; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7;
                                                GENERAL INFORMATION:
APPLICANT: Kilpatrick, David
TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES
TILE REFERENCE: 62242/US
CURRENT APPLICATION NUMBER: US/09/147,933A
CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: PCT/US97/17734
EARLIER FILING DATE: 1997-10-01
EARLIER FILING DATE: 1996-10-02
NUMBER: OF SEQ ID NOS: 96
SOFTWARE: FRACES OF TOWN NUMBER: US. 60/027,353
FARIER PILING DATE: 1996-10-02
NUMBER: OF SEQ ID NOS: 96
SOFTWARE: FRACES OF TOWN NUMBER: DETECTION NUMBER: DETECTION NUMBER: US. 60/027,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 3; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2)...(2)

TOTAL INFORMATION: "RESIDUE 2 = LEU OR MET"

OTHER INFORMATION: peptide
US-09-147-933-35
; Sequence 35, Application US/09147933A; Patent No. 6168917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60, Application US/08666473; Patent No. 5843713; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Score 21; DB 1; Length 5;
Pred, No. 4.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/07657769B
Patent No. 5256766
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
                                                      CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/657,769B

FILING DATE: 19910219

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0502:00

TELEPAATION NUMBER: 29,959

TELEPAATION INFORMATION:

TELEPAATION INFORMATION:

TELEPAATION 1870-1951

TELEPAATION SOR OID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: SEA mino acids

LENGTH: SEA mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWAREN PARENTING STATEMENT OF SOFTWAREN PARENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
ATONEX/AGENT INFORMATION:
NAWE: WITHASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%;
      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AMINO ACID
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MDPTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LDPRP
        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, MAKOA
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
COMRESPONDENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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| Retent No. 2256766
| GENERAL INFORMATION:
| APPLICANT: COUGHLIN, SHAUN R.
| TITLE OF INVENTION: PRECOMBINANT RECEPTOR AND RELATED
| TITLE OF INVENTION: PHARMACEUTICALS
| NUMBER OF SEQUENCES: 69
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: IRELL & MANELLA
| STREET: 545 MIDDLEFIELD ROAD, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 2; Length 7; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                     COMPUTER: REALABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
PILING DATE: 19-SEP-1996
CLASSIFICATION NUMBER: WC/07/996/02238
PILING DATE: 01-NOV-1995
PRIOR APPLICATION NUMBER: WC PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION NUMBER: US/08/666,473
APPLICATION NUMBER: US/08/666,473
PILING DATE: 01-NOV-1995
PILING DATE: 09-FEB-1995
PRIOR APPLICATION NUMBER: 106-269111
FILING DATE: 01-NOV-1994
ATTONNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REBERENCE/DOCKET NUMBER: 16887/837
TELEPRAK: (202)672-5309
TELEPRAK: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202,
TELEX: 904136
INFORMATION FOR SEQ ID NO: 60
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
"VPE: amino acids
"VPE: amino acids
                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy A'
COMPUTER: IPP
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COMPUTER READABLE FORM:
                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AMDPTP 8
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                                                                                                                                                                                        CITY: Washi
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-666-473-60
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STATE:
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Gaps

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US-08-335-198-20
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                                                        Gaps
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Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
COMMESSIONENCE ADDRESS: ADDRESSER: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
                                                                                                                                                                                             US-07-657-769B-62
; Sequence 62, Application US/07657769B
; Patent No. 5226766
; Patent No. 5226766
; Patent No. 5226766
; TITLE OF INVENTION:
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.8%; Score 21; DB 1; Length 5; 60.0%; Pred. No. 4.1e+05; tive 1; Mismatches 1; Indels
                  48.8%; Score 21; DB 1; Length 5; 60.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-0502.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATEH.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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linear
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STRANDEDNESS: Sin
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1 LDPRP 5
                                                                                          4 MDPTP 8
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1 LDPRP 5
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US-08-335-198-20
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Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/07/789,184

FILING DATE: 19911107

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                     APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-034-1991
ATTORNEY AGENT INFORMATION:
NAME: PABEL, PATER L.
REGISTRATION NUMBER: 31,284
; REPERENCE/DOCKET NUMBER: 31,284
; REPERENCE/DOCKET NUMBER: 114(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.8%;
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INPORMATION FOR SEQ ID NO: 68
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MDPTP 8
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                                                  US-08-485-886-68
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                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                          Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                      Score 21; DB 1; Dred. No. 4.1e+05;
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415) 813-5600
TELEPHONE: 415) 494-0792
TELERAX: 415) 494-0792
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 68, Application US/08475263; Patent No. 5759994; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                        48.8%;
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0°
Lag 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                  TOPOLOGY: linear
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LDPRP 5
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TOPOLOGY:
US-08-475-263-68
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Gaps ö 48.8%; Score 21; DB 1; Length 5; 60.0%; Pred. No. 4.1e+05; ative 1; Mismatches 1; Indels Sequence 68, Application US/08485886
Patent No. 5798748
GENERAL INPORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS: Sequence 68, Application US/08477362;
Patent No. 5849507;
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS COUNTRY: CALLEGINGA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDTION TYPE: FORM:
OMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BCS/MS-DOS
SOFTWARE: PATENTIN RC-BCS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,886
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUMBARE: US/07/089,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUMBER: 22,959
REFERENCE/DOCKET NUMBER: 22,959
TELECOMMUNICATION NUMBER: 22,950
TELECOMMUNICATION NUMBER: 22,950

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1; Mismatches

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48.8%; Score 21; DB 2; Length 5; 60.0%; Pred. No. 4.1e+05;
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                                                 SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-477-134-68
                                                                                                                                                                                                                                                                                                                                               3; Conservative
                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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Best Local Similarity
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; TOPOLOGY: linear
US-08-473-489A-68
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1 LDPRP 5
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                                                                                                                                                                                                                                                                                                                                               Matches
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Patent No. 5856448
Patent No. 5856448
Patent No. 5856448
Patent No. 5856448

APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
CORRESPONDENCE ADDRESS: 223
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,362
FILING DATE: 07-JUN-1995
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEXX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LEMGTH: 5 amino acid
TYPE: amino acid
TYPE: Amino acid
TYPE: SINGLE
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CITY: Palo Alto
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
CUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATENTION DATA:
APPLICATION NUMBER: US/08/477,134
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAMME: MUMBER: 22,959
REFERENCE/DOCKET NUMBER: 22,959
REFERENCE/DOCKET NUMBER: 22,959
REFERENCE/DOCKET NUMBER: 22,959
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 60.0
Matches 3; Conservative
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US-08-477-362-68
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1 LDPRP 5
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                                                                                    GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
APPLICANT: SCARBOROUGH, ROBERT M.
TILLE OF INVENTION: RELATED PHARMACEUTICALS
TILLE OF INVENTION: RELATED PHARMACEUTICALS
CORRESPONDENCES: 223
CORRESPONDENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
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ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE:
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/473,489A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB 3; Length 5; Pred. No. 4.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/07/789,184
FILING DATE: 1991-11-07
ATTORNEY/AGENT INFORMATION:
NAMME: MURABHIGE, KATE H.
REGISTRATION NUMBER: 29,959
RESULT 15
US-08-473-489A-68
'S-Quee 68, Application US/08473489A'
Partent No. 6024936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.8%;
Best Local Similarity 60.0%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Tue May 31 05:57:55 2005

- protein search, using sw model OM protein May 26, 2005, 18:26:23 ; Search time 15.8 Seconds (without alignments) 60.897 Million cell updates/sec Run on:

US-10-047-945-1 54

1 LKAMDPTPPL 10 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 8 8 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SIMMARIES

	Description	conserved hypothet	hypothetical prote	딩	similar o transcri	hypothetical prote	alpha-1-B-glycopro	hypothetical prote	hypothetical prote	tailless (tll) pro	tailless (tll) pro	ă						O	hypothetical prote	hypothetical prote	ч	ATP-dependent RNA	DNA-binding protei	probable membrane	TAF25 protein - ye	c	lipoic acid synthe	d hypotl	protein kinase (EC	kinase
SUMMARIES	e e	A81717	T29187	S62497	AE1681	C87585	A42013	S72384	809852	B47265	A35602	T32008	AF3319	C71955	F87552	T29519	T29716	H70986	T49096	T21179	A89624	T46568	A34203	S61040	S50913	E64679	AH2017	A95859	TVMVF6	TVFVMM
	DB	7	~	7	7	~	0	~	~	7	~	7	~	~	~	~	7	~	~	~	~	~	~	~	N	N	N	~	-	н
	Length	398	792	1325	142	212	237	286	429	450	452	1819	117	222	365	392	431	460	490	868	944	968	2717	159	206	262	291	313	323	380
d	Query Match	77.8	70.4	70.4	68.5	68.5	68.5	68.5	68.5	68.5	68.5	68.5	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	9	64.8	4.	64.8	64.8	64.8	64.8	64.8
	Score	42	38	38	37	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	35	35	35	35	35	35	35
	Result No.		7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

protein kinase (BC	protein kinase (EC	probable protein k	Cytochrome P450-EF	succinate dehydrog	protein kinase (EC	hypothetical prote	protein kinase raf	protein kinase raf	protein kinase raf	beta-glucuronidase	protein p84 - huma	probable vacuolar	chitinase - Strept	immediate-early pr	hypothetical prote
TVBEG1	TVBEKA	T42612	A53790	I40849	TVRTRR	T18772	S00644	TVHUF6	TVRTRF	A25047	A53545	T50256	T35719	EDBEXD	T46354
н	Н	~	~	~	Н	~	н	-	-	~	~	~	~	ч	7
382	382	384	543	587	602	627	647	648	648	648	657	678	765	825	1397
64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

		muridar	
		Chlamydia	10000
		١	1
		[imported]	Charles able
		TC0306	1
		protein	m. 40
		served hypothetical protein TC0306 [imported] - Chlamydia muridar	socioni Ohlamidia ministratura Ohlamidia tanathemetic Ment
JLT 1	717	served	

um (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

Cipacesion: A81117
RiRead, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 139-1406, 2000, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255; PMID:10684935
A; Accession: A81717
A; Residues preliminary
A; Molecule type: DNA
A; Residues: 1-398 <TETA
A; Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A; Experimental source: strain Nigg (MoPn)

A;Gene: TC0306 C;Superfamily: Chlamydia trachomatis hypothetical protein CT036

Length 398; 77.8%; Score 42; DB 2; 77.8%; Pred. No. 8.4; Query Match

Gaps ö 1; Indels Pred. No. 8.4; 1; Mismatches Conservative Local Similarity hes 7; Conserv Best Loc Matches

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| :|||||| KELDPTPPL 317 2 KAMDPIPPL 10

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hypothetical protein C55C3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T29187

Riwoessne, J.; Stellyes, L. submarted to the EMBL Data Library, April 1996 A; Description: The sequence of C. elegans cosmid C55C3. A; Reference number: Z20585

A;Accession: T29187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-792 <WOE>
A;Cross-references: EMBL:U53335; PIDN:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3
A;Experimental source: strain Bristol N2; clone C55C3

C;Genetics:

A; Gene: CESP: C55C3.3

A;Map position: 4 A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43

Length 792; 70.4%; Score 38; DB 2; Query Match N

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Cyaccesion: C87585

Cyaccesion: C87585

R; Micraman, W.C.; Feldhyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-1-B-glycoprotein - North American opossum (fragments)
Cspecies: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C;Date: 10-11922 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricatanese, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum
A;Reference number: A42013; WUID:92118834; PMID:1731898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 8 precursor - Enterococcus faecalis plasmid pAD1
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: 572384
R;Hirt, H.; Wirth, R.; Muscholl, A.
Mol. Gen. Genet. 252, 640-647, 1996
A;Title: Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: C,A;Reference number: 872375; MUID: 9974879; PMID: 8917306
A;Accession: 572384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9A4W1; GB:AE005673; NID:g13424303; PIDN:AAK24679.1; GSPDB:C
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                                                                                                                                                                                                       hypothetical protein CC2714 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB Pred. No. 32; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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A,Molecule: type: mRNA
A,Resiue: 1-27 < CAT>
A,CCOSS-references: UNIPROT:Q28359; GB:J05356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                       130 LKEMDPTKP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CC2714
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C;Dates: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1681
E;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
F;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
F; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jonnes, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Acteus: preliminary
A;Molecule type: DNA
A;Residues: 1-142 < Glass
A;Residues: 1-142 < Glass
A;Resimental source: strain Clip11262
C;Genetics:
C;Genetics:
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lini1991
C;Superfamily: conserved hypothetical protein MJ0568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S62497
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1325 <NIB>
A;Cross-references: UNIPROT:Q09847; EMBL: Z64354; NID:g1039338; PIDN:CAA91241.1; PID:g103
B;Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar o transcription regulators lin1991 [imported] - Listeria innocua (strain Clip114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: 22783
A;Accession: T38281
A;Accession: T38281
A;Actual T38281
A;Actual type: DNA
A;Residues: 1-1325 <NI2>
A;Cross references: EMBL:Z64354; PIDN:CAA91241.1; GSPDB:GN0066; SPDB:SPAC23D3.06c
C;Genetics:
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                                    ö
                                                                                                                                                                                                                                                                                 probable nucleoporin - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62497; T38281
R;Niblett, D.; Harris, D.
R;Niblett, D.; Harris, D.
R;Niblett, D.; Harris, D.
A;Reference number: S62492
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                                    Indels
                                    1;
      Pred. No. 93;
0; Mismatches
87.58;
   Best Local Similarity 87.5
Matches 7; Conservative
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133 LKPMDPTP 140
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                                                                                         1 LKAMDPTP
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Gene: SPAC23D3.06c
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Lailess (tll) protein - fruit fly (Drosophila melanogaster)
N;Alternate names: steroid hormone receptor homolog tll; transcription factor tll
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35602; A47265
R;Pignoni, F.; Baldarelli, R.M.; Steingrimsson, E.; Diaz, R.J.; Patapoutian, A.; Merriam A;File: The Drosophila gene tailless is expressed at the embryonic termini and is a mem A;Reference number: A35602; MUID:90304905; PMID:2364433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc finger F;32-341/Domain: erbA transforming protein homology <ERBA>
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A;Molecule type: DNA
A;Residues: 1-1819 < DBA>
A;Residues: 1-1819 < DBA>
A;Cross-references: UNIPROT:016625; EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone K10G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-452 <LIA>
A;Cross-references: GB:AF019362; GB:L04954; NID:g2429340; PIDN:AAB71371.1; PID:g2440022
A;Note: sequence extracted from NCBI backbone (NCBIN:124057, NCBIP:124058)
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribiaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A. Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
A.fitle: Characterization of Gownstream elements in a Raf-1 pathway. A;Reference number: A47265; MUID:93157371; PMID:8430097
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A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
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R;Davidson, S.; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid KlOG6.
A;Reference number: Z21111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein K10G6.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNĀ
A;Residues: 1-452 <PIG>
A;Cross-references: UNIPROT:P18102; GB:X52147
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A;Cross-references: FlyBase:FBgn0003720
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216 RALPPTPPL 224
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218 RALPPTPPL 226
                    2 KAMDPTPPL 10
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C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Accession: S09852
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrell, B.G.
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09749; MUD: 90269039; PMID: 2161319
A;Reference number: S09749; MUD: 90269039; PMID: 2161319
A;Accession: S09882
A;Accession: S09882
A;Accession: B088
A;Accession: UNIPROT: P16711; EMBL: X17403; NID: 959591; PIDN: CAA35362.1; PID: 917808
A;Cross-references: UNIPROT: P16711; EMBL: X17403; NID: 9brary, December 1989
A;Residues: 1-286 <hr/>
A;Cross-references: UNIPROT:Q47791; EMBL:X96977; NID:g1279406; PIDN:CDA65667.1; PID:g127
A;Cross-references: UNIPROT:Q47791; EMBL:X96977; NID:g1279406; PIDN:CDA65667.1; PID:g127
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics: plasmid pADI
C;Superfamily: probable pheromone-responsive protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-286/Product: hypothetical protein 8 #status predicted <MAI>
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C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: B47265
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
A;Title: Characterization of downstream elements in a Raf-1 pathway.
A;Reference number: A47265; MUID:93157371; PMID:8430097
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Pred. No. 44;
1; Mismatches 2; Indels
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C;Superfamily: erbA transforming protein homology
C;Keywords: zinc finger
F;32-339/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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A;Molecule type: DNA
Residues: 1-450 <LIA>
A;Cross-references: GB:L04955
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DPTPPL 296
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                    Accession: AF312

Approach of VG.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A; Reference number: AD3252; PMID:1175688
A.Accession: AF319
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-117 < kUR>
A.Residues: 1-117 < kUR>
A.Experimental source: strain 16M
A.Experimental source: strain 16M
A.Experimental source: strain 16M
A.Map position: I
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R;Accession: C71955
R;Alm, R.A.: Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A;Status: preliminary
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87552
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B;Nierman, W.C.; Peldblyum, T.V.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT;Q9ZMH9; GB:AE001462; GB:AE001439; NID:g4154760; PIDN:AAD0583
A,Experimental source: strain J99
C,Genetics:
A,Gene: jhp0241
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A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                         Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                   hypothetical protein BME10540 [imported] - Brucella melitensis (strain 16M)
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Pred. No. 24;
1; Mismatches
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Pred. No. 50;
0; Mismatches
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75.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conserv
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A; Residues: 1-222 <ARN>
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n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87552
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9A5KO; GB:AE005673; NID:g13423992; PIDN:AAK24418.1; GSPDB:GG;Genetics:
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A;Experimental source: strain Bristol N2; clone T25F10
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C; Date: i5-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Map position: 5
A;Introns: 38/3; 84/2; 156/3; 182/3; 228/3; 256/1; 312/2; 337/3; 361/2
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submitted to the EMBi Data Library, July 1996
A;Description: The sequence of C. elegans cosmid T25F10.
A;Reference number: 220634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T25F10.4 - Caenorhabditis elegans
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A,Molecule type: DNA
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100.0%; Pred. No. 95;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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drosophila drosophila neurospora

enterococcu enterococcu enterococcu enterococcu didelphis m rhodopseudo

Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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MEDINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0; Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.; "Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae."; Toxicon 32:1237-1249(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Metatheria, Didelphianorphia, Didelphidae, Didelphis.
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Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
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28-FRB-2003 (Rel. 41, Last sequence update)
28-UJL-2004 (Rel. 44, Last annotation update)
Venom metalloproteinase inhibitor DM43.
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Q838G9
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Q9F1F9
Q82YS6
Q8HYX5
Q6NAYS
Q0NAS0
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Best Local Similarity 100.
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DT 28-PEB-DT 05-UUL-
DE Venom n 05-UUL-
RP SEQUENC RT ISSUES
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                                                                                                                                                    May 26, 2005, 18:18:07; Search time 76.4 Seconds (without alignments) 67.026 Million cell updates/sec
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Q9a4w1
Q8bxk6
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Q8hz74
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Q6nvj6
Q6fvq3
Q95qq6
Q8cba3
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                       5.1.6
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                        1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                       GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y306_CHLMU
QQCS47
QQCS47
QQCS347
QQES347
QQES347
QQENLX6
QQENLX6
QQENLX6
QQEQ1P6
QQEQ1P6
QQEQ1P6
QQENV3M1
QQECD43
QQECD63
QQEC
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Q8HZ75
Q8HZ74
Y306_CHLMU
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Match Length DB
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54
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Score

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Result

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Gaps

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Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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Best Local Similarity 77.87
Lan 7; Conservative
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                 NCBI_TaxID=9267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
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Q9PL02;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha 1B glycoprotein DVOP51-D (Fragment).
Didelphis marsubialis virginiana (North American opossum).
Eukaryota, Metazoa; Chordata; Verteniata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                         (Potential)
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                                        NOTE-Ref.l.
-!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
                   MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1; Length 291; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martinez M.E., Pierce J.R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY131000; AAN06911.1; -.
HSSP, 076036; 10LL.
                                                                                                                                                                                                                                                                                                                                                                          17A496227E69A65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA; 15297 MW; E19D071A76AA5A7F CRC64;
                                                                                                                                                                                                                                                                                                                    (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                  Ig-like V-type 1.
Ig-like V-type 2.
Ig-like V-type 3.
                                                                                                                                                                                                                                                                                                                                                       (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                  N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                       N-linked
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                                                                                                                                                                                                                                                                                                                                                       175 N
32390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTPPL 10
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42 LKAMDPTPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                         DISULFID
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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MEDLINB=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
MCClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the chlamydial CPn0129/CT036/TC0306 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia muridarum.
Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                            Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY131001; AAN06912.1; -.
HSSP; QBNIL6; 1G0X.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
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TRANSMEM 31 51 Potential.
TRANSMEM 56 76 Potential.
                                                                                                                                                                                                                                                                                                                         291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8CD8E541C5C92A88 CRC64;
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Pred. No. 66;
1; Mismatches

    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 2
Pred. No. 14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                  83.3%;
90.08;
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OrderedLocusNames=TC0306;
                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPL 10
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                                                                                                                                                                           Pfam; PF00047; 19; 1.
SMART; SM00409; IG; 1.
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Gaps

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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangell L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Mincker P., Souciet J.L.,
"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gabs
                                                                                                            25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sgd|S0007245 Saccharomyces cerevisiae YLL018ca COX19.
ORFNames=KLLA0D03971g;
                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=284590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.9%; Score 41; DB 2; Length 99; 77.8%; Pred. No. 21; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382124; CAH00338.1; -. InterPro; IPR010625; CHCH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                         99 AA.
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                                                                                                                                                                         Kluyveromyces lactis NRRL Y-1140.
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01-MAY-2000 (TrEMBLrel. 13, C;
01-MAY-2000 (TrEMBLrel. 13, L;
25-OCT-2004 (TrEMBLrel. 28, L;
CG2147-PA (LP02728P).
ORFNAMES=CG2147;
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                                                                                         PRELIMINARY;
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                      309 KELDPTPPL 317
        2 KAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 430:35-44(2004)
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LKALSPTPP 17
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=NRRE Y-1140;
                                                                                                                                                                                                                                                            Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
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                                                                                                     Q6CS47;
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Matches
                                                                 RESULT 6
Q6CS47
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Q9W3H5
LD Q9W3H5
AC Q9W3J
DT 01-M
DT 01-M
DT 25-00
DE CG21.
GN ORFN
OC BUASA
OC EUASA
OC EDASA
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RAMINIANCE FROM N. Aughded 17711127, 2017. 1128/science.29.1461.2185;
RAMINIANCE FROM N. Aughded 177. 21499 C. Chen L.Y.
RAMINIANCE FROM N. Scherer 28. L. 16 P. W. Devan 2. C. Chen L.Y.
RAMINIANCE C.S. Scherer 28. L. 16 P. W. Devan 2. C. Chen L.Y.
RAMINIANCE C.S. Scherer 28. L. 16 P. W. Devan 2. C. Chen L.Y.
RAMINIANCE C.S. Scherer 28. L. 16 P. W. Devan 2. C. Chen L.Y.
RESIDER C. S. Scherer 28. L. 16 P. W. Devan 2. C. Chen L.Y.
RESIDER C. S. Scherer 28. L. 16 P. W. Devan 2. C. C. Baldwin D. Beasley E. W.
RESIDER C. S. Scherer 28. L. 16 P. W. Devan 2. C. C. Baldwin D. Beasley E. W.
RESIDER C. S. Scherer 28. L. 16 P. W. Devan 2. C. Scherer 28. P. Chantz 1.
RAM K. H., Doyle C. Backer 28. R. 16 P. Bercher 28. P. Chantz 1.
RAM C. Decchan M.Y. Bould J. Bercher 28. P. Bercher P. S. Devan 3. W.
RESIDER C. C. Scherer 28. P. Bercher 28. P. Devan 3. W.
RAM C. C. Scherer 29. Devan 3. W. Devan 3. W. Devan 3. W. Devan 3. W. Cawley S. Devan 3. W. Devan 3.
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Homo sapiens (Human).
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SEQUENCE 227 AA,
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05-JUL-2004
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0961D3
1D 0961D
DT 01-DE
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OS HOMO
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MEDILINE-2259566; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
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                                                                                                                                                                                                                                         STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Mixanda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Ebbatta A., Maragall C.D., Ball, Genbank/DDBJ databases.
EMBL; AR00343; AAR46352.1; -
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=205877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%; Score 39; DB 2; Length 98; 75.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                        FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIYBase, FBGN0030025, CG2147.
SEQUENCE 165 AA; 17157 MW; CF3E6D2E102302C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Origins of highly mosaic mycobacteriophage genomes."; cell 113:171-182(2003) EMBL, AV129337, AAN16740.1; -SEQUENCE 98 AA, 10867 MW, DID8FE87C4CDD15E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ntAct; Q9W3H5; -
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Q8MLX6
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X MEDLINE=22060722; PubMed=12065546;
X MEDLINE=22060722; PubMed=12065546;
X MEDLINE=22060722; PubMed=12065546;
X MEDLINE=22060722; PubMed=12002;
Dol=10.1128/III.70.7.3969-3972.2002;
A Gauci C., Merli M., Muller V., Chow C., Yagi K., Mackenstedt U.,
I Lightowlers M.W.;
Molecular cloning of a vaccine antigen against infection with the large of Echinococcus multilocularis.";
Infect. Immun. 70:3969-3972(2002).
Infect. Immun. 70:3969-3972(2002).
RBBL; AY062921; AAL51153.1;
RBBL; AY062921; AAL51153.1;
RBBL; AY062921; FN III.
NR InterPro; IPR003961; FN III.
NR InterPro; IPR003961; FN III.
NR RRART; SM00060: FN3; 1.
NR PROSITE; PSS0853; FN3; 1.
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EMBL; AE017233; AAS04008.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 227;
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70.0%; Pred. No. 1.2e+02;
tive 1; Mismatches 2; Indels
                                                                           Eukaryota; Metazoa; Platyhelminthes; Cestoda; Bucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
KIAA1115 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 2; 70.0%; Pred. No. 76; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 AA
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                                EM95 vaccine antigen.
Echinococcus multilocularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames=MAP1691c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
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Name=SPV074;
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Q9K437;
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                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H.,
Canbaeck B., Eriksson A.-S., Naselund A.K., Handley S.A., Huvet M.,
La Scola B., Holmberg M., Andersson S.G.B.;
"The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zonorcic agent Bartonella henselae.";

EMBL: BX897699; CAF28391.1; -.
EMBL: BX897699; CAF28391.1; -.
GO; GO:0008415; F.acqltransferase activity; IEA.
GO; GO:00152; P.metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                        Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                     Length 243;
                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
BRBL; BC007629; AAH07629.1; -.
                                                                                                                                                                                                                                                                                                                  243 AA; 24559 MW; 9094604DE4A93228 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                    72.2%; Score 39; DB 2; I 66.7%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-acyl-sn-glycerol-3-phosphate acyltransferase.
                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002123; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 49882 / Houston 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bartonellaceae; Bartonella.
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Best Local Similarity 66.7
Lag 6; Conservative
                                                                                                                                                                                                                                and mouse cDNA sequences.
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130 LRSQDPTPP 138
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                             Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                            Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 320;
                                                                                         Score 39; DB 2; Length 200. Pred. No. 1.46+02;
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GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0016855; F:isomerase activity; IEA.
GO; GO:0016265; F:DNA topological change; IEA.
GO; GO:0016268; F:DNA unwinding; IEA.
PF01028; Topoisom I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Pfam; PP01553; Acyltranaferase; 1.
SMART; SM00563; PlBC; 1.
Acyltranaferase; Complete proteome; Tranaferase.
SEQUENCE 268 AA; 30957 MW; 2P955B7EEFBDBB95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AA; 38179 MW; 97F9B94442DD1DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00176; TOPOISOMERASE I EUK; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomycee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; I
Pred. No. 1.7e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                 320 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 76:/b3-/20.20.
EMBL; AF410153; AAL69813.1; -.
HSSP; P08585; 1VCC.
                                                                                                            Query Match 72.2%;
Best Local Similarity 77.8%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0416; EUTPISMRASEI
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match
Best Local Similarity 50.vv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPV074 DNA topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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241 IKSLDPVPPI 250
                                                                                                                                                                                                                                                240 LAAQDPTPP 248
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                                                                                                                                                                                                     1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=SCG22.08c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suipoxvirus.
NCBI_TaxID=10276;
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Search completed: May 26, 2005, 18:43:17
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EMBL; AL939107; CAB95281.1; -...

EMBL; AL939107; CAB95281.1; -...

EMBL; AL939107; CAB95281.1; -...

GO, GO:00167807; Fihydrolase activity, IEA.

GO; GO:0005975; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR006101; Glyco.hydro.21g.

InterPro; IPR006102; Glyco.hydro.21g.

InterPro; IPR006104; Glyco.hydro.22B.

InterPro; IPR006109; Glyco.hydro.22B.

InterPro; IPR006109; PPTA.
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MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
HOpkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:197-205(1999).
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Ruters S., Seeger K., Saunders D., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hydrolase. – SEQUENCE 693 AA; 75941 MW; E54676BCCA33A921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UPN7; Q9BU97;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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Pfam; PF0283; Glyco hydro 2; 1.
PRIMTS; PF02837; Glyco hydro 2N; 1.
PRIMTS; PR00132; GLHYDRLASE2.
PROSITE; PS00904; PPTA; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99397452; PubMed=10470851;
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Matches 7; Conservative
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420 LKALDPTRPV 429
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                                                                                                                                                                                                                                 Hopwood D.A.;
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KB15, HUMAN

AC 09UPN7,

28-PEB

DT 28-PEB

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Poly-Glu.
P -> S (in Ref. 1).
9 BB6964AE2226774E CRC64;
                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the SAPS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glu-rich.
Pro-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intact; O9UPN7; -. Genew, HGNC:29195; KIAA1115. InterPro; IPR007587; SAPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 66.7
Matches 6; Conservative
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DOMAIN
CONFLICT
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                                                                                                                                               May 26, 2005, 18:17:22; Search time 86 Seconds (without alignments)
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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	44.972 Million cell updates/sec
Title:	US-10-047-945-1
Seguence:	54 1 LKAMDPTPPL 10
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues
Total number of	Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* A_Geneseq_16Dec04: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:*

geneseqp2003as:*geneseqp2003bs:*

SUMMARIES æ

no i tri i tra e l		Aaw53843 N-terminu	Abb80222 Synthetic	Abb80226 Synthetic	Abb80225 Synthetic	Aaw11575 N-termina	Aaw53841 N-terminu	Abb80223 Synthetic	Abb80227 Synthetic	Abb80228 Synthetic	Aao02179 Human pol	Abb58900 Drogonil	Aab59012 Breagt an	Abm82174 Tumour-as	Ads88328 Human pro	Aam85892 Human imm	Abm74107 DNA clone		Arabid	Aag47069 Arabidops	Aag24233 Arabidops	Abb93666 Herbicida	Aag47028 Arabidops	Aaw39043 Peptide r	Aay00125 Enterococ	Abra3344 R faecali
		AAW53843	ABB80222	ABB80226	ABB80225	AAW11575	AAW53841	ABB80223	ABB80227	ABB80228	AA002179	ABB58900	AAB59012	ABM82174	ADS88328	AAM85892	ABM74107	AAY43943	AAG17097	AAG47069	AAG24233	ABB93666	AAG47028	AAW39043	AAY00125	ARP43344
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Result			8	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

Claim 7; Col 11; 11pp; English.

mmm			Abb58056 Drosophil Adn25164 Bacterial Abg17160 Novel hum Adf60462 Human con	Aao09783 Human pol Aao06147 Human pol Abm82179 Tumour-as	Abg26257 Novel hum Aaw55552 H. pylori Abo67138 Klebsiell
ABU88372 ABU13623 AAY00124	ABP43343 ABU88371 ABU13622 ABU29194	ABU28946 ADH88791 ADH88698	ABB58056 ADN25164 ABG17160 ADF60462	AAO09783 AAO06147 ABM82179	ABG26257 AAW55552 ABO67138
9981		9 7 7	4047	440	4 10 L
210 210 256	256 256 256 270	285 291 306	452 481 86 86	100 107 172	220 222 323
688 68.5 68.5 68.5	68.5 68.5 68.5 68.5	68.5 68.5 68.5	68.5 68.5 66.7	66.7 66.7 66.7	66.7 66.7 66.7
37	37 37 37	37	37 36 36	36 36 36	36 36
26 27 28 28	3378	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9 B B B B B B B B B B B B B B B B B B B	4 4 4 0 1 2	4 4 4 5 5

## ALIGNMENTS

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LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; attl-haemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                     Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
       AAW53843 standard; peptide; 10 AA.
                                                                                                                                                                                       96US-00657163.
                                                                                                                                                                                                         93US-00058387.
                                                                N-terminus of opossum LINF.
                                              (first entry)
                                                                                                                                Didelphis virginiana
                                                                                                                                                                                                                                                                Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                    WPI; 1998-271108/24.
                                                                                                                                                                                                                                    (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                      03-JUN-1996;
                                                                                                                                                                                                         10-MAY-1993;
22-SEP-1994;
                                              08-JUL-1998
                                                                                                                                                  US5744449-A.
                                                                                                                                                                     28-APR-1998.
                           AAW53843;
AAW53843
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLDE), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves, disease, atthritis, syndrome, Reiter's syndrome, The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of the protein in the contact of the protein.
                                                                                                                                                      0;
snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; 1gE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjongren 8 syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clotting time before centrifugation to separate form. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                      Gaps
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                                                                                                                                                      ;
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                                                                                                             Length 10;
                                                                                                                                                    0; Indels
                                                                                                                 Score 54; DB 2;
Pred. No. 0.033;
                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                       ABB80222 standard; peptide; 10 AA.
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                                                                                                               100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                         Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                         10
                                                                                                                                                                                                                           LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic LTNF, LT-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipps BV, Lipps FW;
                                                                                                                                                                                         1 LKAMDPTPPL
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                                       to horse proteins
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                                                                            Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         saliva; ELISA
                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (19E), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and triansteing conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva caple using an anti-serum that is specific for the protein. Saliva can be centrifuged immediately, whereas blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                100.0%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
                                                             100.0%; Pred. ...
                                                                                                                                                                                                                                                  ABB80226 standard; peptide; 11 AA.
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                                                                                      10; Conservative
                                                                                                                          1 LKAMDPTPPL 10
                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                           Synthetic LTNF, LT-11.
                                                                                                                                                           1 LKAMDPTPPL
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                                                 Query Match
Best Local Similarity
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                  Sequence 10 AA;
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Sequence 11 AA;

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, attoinmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, addison's disease, or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a salive collection is relatively non-invasive when compared to blood collection of for serum. Salive can be centrifiged immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                                                                   IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; Abb; asthma; diabetes; autoimmune disease; syetemic lugus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                                                                                                                                                                                                                                                Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clotting time before centrifugation to separate serum. Saliva proteins
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an BLISA on a saliva sample from a
                                                          ö
                    Length 11;
                                                        0; Indels
                  100.0%; Score 54; DB 7; 100.0%; Pred. No. 0.036;
                                                        Mismatches
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                                                                                                                                                                                                                                                                                           (first entry)
                                                          Conservative
                                                                                         1 LKAMDPTPPL 10
                                                                                                              Synthetic LTNF, LT-12.
Ouery Match
Best Local Similarity
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LIPPS F W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        saliva; ELISA.
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                                                                                                    Lethal toxin neutralising factor, LTNF, opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
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                                                                                                                                                                                                         N-terminal peptide from lethal toxin neutralising factor.
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                                                                                                  AAW11575 standard; peptide; 15 AA.
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                                                                                                                                                                             (first entry)
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LKAMDPTPPL 10
                           LKAMDPTPPL 10
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                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                 Didelphis virginiana.
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                                                                                                                                                             25-MAR-2003
20-MAR-1997
                                                                                                                                                                                                                                                                                                                                          19-NOV-1996.
                                                                                                                                 AAW11575;
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Gaps

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100.0%; Score 54; DB 7; Length 12; 100.0%; Pred. No. 0.039; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 10; Conservative

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MCP), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and traticular, the methods of the invention are useful for diagnosing and arthritis, conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva con ecentrifugation to separate serum. Saliva proteins con be centrifugation to separate serum. Saliva proteins can be assayed by a simple BLISA test, whereas an assay of proteins from a be assayed by a simple BLISA test, whereas an assay of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                       Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 54; DB 7; Length 15; 100.0%; Pred. No. 0.049; cive 0; Mismatches 0; Indels
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                                                                                                                          14-JAN-2003; 2003WO-US001044
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Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                      Lipps BV, Lipps FW;
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                          WO2003060471-A2
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                                                                           24-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidee, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of so or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                            LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorxhagto protein; Blappidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; hab, asthma; diabetes; autoimmune disease; systematic lugum erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80223 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 11; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                               93US-00058387
94US-00310340
                                                                                                                                                                                                                                                                                                                                96US-00657163
N-terminus of opossum LINF.
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                                                                                                                                                                            Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-271108/24
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Best Local Similarity
Matches 10; Conserv
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LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                  LO-MAY-1993;
                                                                                                                                                                                                                             US5744449-A.
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Gaps

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WO2003060471-A2

Synthetic

saliva; ELISA

ABB80223;

RESULT 7 ABB80223

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8

Best Loca Matches

Synthetic

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patient.
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                                                                                                                                                                                                                                                The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (1g8), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Relier's Syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzymenitored by assaying a human endogenous protein by performing an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of the protein saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection con be centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.6%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                            Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2003; 2003WO-US001044.
                        14-JAN-2003; 2003WO-US001044
                                                 14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.
9; Conservative
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                                                                                                             Lipps BV, Lipps FW;
                                                                                                                                      WPI; 2003-636703/60.
                                                                       (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
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24-JUL-2003
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Best Local S
                                                                                                                                                                                                     patient.
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addisease or Hödgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                  e.g.
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                                                                                                                                                                                                                                                                                             Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 7; Le
Pred. No. 1.8e+06;
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100.0%; Pred. No.....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 4; 24pp; English.
14-JAN-2002; 2002US-00047945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                    Lipps BV, Lipps FW;
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nes 8; Conserv
                                                               (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Gaps

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Length 165; 0; Indels

Tang YT,

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic, neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Breast and ovarian cancer associated antigen protein sequence SEQ ID 720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                  75.9%; Score 41; DB 4;
100.0%; Pred. No. 73;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1174-1176; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB59012 standard; protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US005881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MDPTPPL 10
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                                                                                                                                                                                                                                                                                      Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200055173-A1.
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                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to gryckine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. atem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                Claim 20; SEQ ID NO 16071; 1399pp + Sequence Listing; English.
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB58900 standard; protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                      Drmanac RT;
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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48 LKSQDPTPP 56
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N-PSDB; ABL03003.
                                                                                 2001-514838/56
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                                   Liu C,
                                                                                                           N-PSDB; AAI82110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 94 AA;
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ABB58900;

RESULT 11 ABB58900

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antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide magnences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target (TAT) polypeptide PRO83096, SEQ:5611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                             Length 459;
                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                         Score 39; DB 3; I
Pred. No. 4.3e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM82174 standard; protein; 754 AA.
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                           346 LRSQDPTPP 354
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                                                                                                                                                                                                 infectious diseases
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                     Sequence 459 AA;
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molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, covarian cancer, liver cancer, bladder cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein of a TNF-alpha signalling pathway protein complex Seq 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bauch A, Ruffner H, Bauer A, Kuester B;
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                                                                                                                                                                                                                                                                                                    Length 754;
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Pred. No. 7.1e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                  72.2%;
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2000US-0241809P.
2000US-0241826P.
2000US-0244617P.
2000US-0246474P.
2000US-0246475P.
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2000US-0229345P.
2000US-0229509P.
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2000US-0241786P.
2000US-0241787P.
2000US-0241808P.
                                                2000US-0226868P.
2000US-0227182P.
2000US-0227009P.
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2000US-0231243P.
2000US-0231244P.
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2000US-0229287P.
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2000US-0230438P.
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2000US-0233064P.
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2000US-0246523P.
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2000US-0246532P.
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                                               22-AUG-2000; 2
22-AUG-2000; 2
23-AUG-2000; 2
30-AUG-2000; 2
01-SEP-2000; 2
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
   14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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20-OCT-2000;
20-OCT-2000;
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08-NOV-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
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13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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20-OCT-2000;
20-OCT-2000;
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21-SEP-2000;
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25-SEP-2000;
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29-SEP-2000;
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02-OCT-2000;
     rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirhematic, cytostaric and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway
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                                                                                                                                                                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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                                                                                                                                                                       Score 39; DB 8; Length 754;
Pred. No. 7.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen SEQ ID NO:13485.
                                                                                                                                                                                                                                                                                                  AAM85892 standard; protein; 78 AA
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16-MAR-2000; 2000US-0189874P.
18-APR-2000; 2000US-01998123P.
19-MAY-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0205515P.
28-JUN-2000; 2000US-021548FP.
30-JUN-2000; 2000US-021647P.
07-JUL-2000; 2000US-021648PP.
11-JUL-2000; 2000US-021829P.
11-JUL-2000; 2000US-021829P.
14-MUG-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0224519P.
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2000US-0225447P.
2000US-0225757P.
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                                                                                                                                                                       Query Match 72.2%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                     1 LKAMDPTPP 9
                                                                                                                              the invention
                                                                                                                                                    Sequence 754 AA;
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14-AUG-2000;
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24-FEB-2000;
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70.4%; Score 38; DB 4; Length 78; 70.0%; Pred. No. 1.1e+02; ive 1; Mismatches 2; Indels
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                      17-NOV-2000; 2000US-0249207P.

17-NOV-2000; 2000US-0249208P.

17-NOV-2000; 2000US-0249208P.

17-NOV-2000; 2000US-0249210P.

17-NOV-2000; 2000US-0249211P.

17-NOV-2000; 2000US-0249211P.

17-NOV-2000; 2000US-0249213P.

17-NOV-2000; 2000US-0249213P.

17-NOV-2000; 2000US-0249213P.
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2000US-0249265P.
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2000US-0250160P
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DEC-2000; 2000US-0256719P
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Best Local Similarity 70.0
Matches 7; Conservative
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N-PSDB; AAK58673.
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17-NOV-2000; 2
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17-NOV-2000;
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manion acid sequences given in AMM81210 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymuclostides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expression patient's genome the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-detived cells. AAK84703 to AAK87694 represent human immune/haematopoietic article antigen genomic sequences from the present invention. AAK84921 to AAK87691 and AAM82169 represent sequences used in the exemplification of the present invention
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                        AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                            Claim 11; SEQ ID NO 13485; 3071pp + Sequence Listing; English.
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Search completed: May 26, 2005, 18:36:48 Job time : 90 secs

1 LKAMDPTPPL 10

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 1, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 253125,	Sequence 133945,	Sequence 162813,	Sequence 162816,	Sequence 720, App	Sequence 720, App	Sequence 51220, A
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. DI	US-10-047-945-1	US-10-047-945-5	US-10-047-945-4	US-10-047-945-2	US-10-047-945-6	US-10-047-945-7	US-10-424-599-253125	US-10-437-963-133945	US-10-437-963-162813	US-10-437-963-162816	US-09-925-298-720	US-10-102-806-720	US-10-767-701-51220
	14	14	14	14	14	14	12	16	16	16	6	14	16
% Query Match Length DB	10	11	12	15	6	œ	80	148	169	206	459	459	75
% Query Match	100.0	100.0	100.0	100.0	92.6	79.6	75.9	75.9	72.2	72.2	72.2	72.2	70.4
Score	54	54	54	54	20	43	41	41	39	. 39	39	39	38
Result No.	П	8	m	4	ß	9	7	80	σ	10	11	12	13

Sequence 138037, Sequence 1996, Ap Sequence 1997, Ap Sequence 144, App Sequence 15816, Sequence 273019,	Sequence 232, App Sequence 232, App Sequence 232, App Sequence 179361,	Sequence 230, App Sequence 230, App Sequence 57118, A Sequence 56870, A Sequence 146546	Sequence 68941, Ap Sequence 68941, Ap Sequence 127940, Sequence 13540, Sequence 280103,	19043 8979, 56593 62510 6365, 64604 16637 3148, 18140
US-10-437-963-138037 US-10-732-923-1996 US-10-732-923-1997 US-10-161-791-444 US-10-424-599-173019			US-1 US-1 US-1 US-1	US-1 US-1 US-1 US-1 US-1 US-1
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#### ALIGNMENTS

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MESULI 1.  Sequence 1, Application US/10047945  Publication No. US2003015755A1  Publication No. US2003015755A1  GENERAL INFORMATION:  APPLICANT: LIPPS, BINIE V.  APPLICANT: LIPPS, FREDERICK W.  TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR TITLE OF INVENTION: UGBS) IMPLICATED DISORDERS FILE OF INVENTION: UGBS) IMPLICATED DISORDERS:  FILE REFERENCE: FWLPATO15US  CURRENT PAPLICATION NUMBER: US/10/047,945  CURRENT PAPLICATION NUMBER: 2002-01-14  PRIOR APPLICATION NUMBER: 2002-01-14  PRIOR APPLICATION NUMBER: 100 TYPE: NUMBER OF SO, ID NO. 1  LENGTH: 10  TYPE: RPT  ORGANISM: Artificial Sequence  FRATURE: NAME: NAME/KRY:	LOCATION: COTHER INFOR COTHER INFOR	Query Match Best Local Similarity Matches 10; Conserv
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                                Sequence 5, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (19E) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
PRIOR PLING DATE: 2002-01-14
PRIOR PLING DATE: TOOS: 7
SOFTMARE: WORDPERFECT 5.1 FOR WINDOWS
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Publication No. US20030157555A1
GENERAL INFORMATION:

APPLICANT: LIPPS, FRIDENCK W.
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
FILE REFRENCE: FWLPPATION: (1GE) IMPLICATED DISORDERS
FILE REFRENCE: FWLPPATION: (1GE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT ALING DATE: 2002-01-14
PRIOR FILING DATE:
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LENGTH: 12
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Matches 10; Conservative 0
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Matches 10; Conservative 0
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US-10-047-945-4
RESULT 2
US-10-047-945-5
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LENGTH: 11
TYPE: PRT
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) Publication No. US20030157555A1
) GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10047945;
Sequence 6, Application US/10047945;
Publication No. US2003015755A1;
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E;
TITLE OF INVENTION: LIPPS IMPLICATED DISORDERS;
FILE REFERENCE: FWLPATO15US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0:
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Pred. No. 1.3e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: SYNTHESIZED. ) OTHER INFORMATION: US 5,576,297. US-10-047-945-2
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; OTHER INFORMATION: Synthetic.
US-10-047-945-6
                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 9; Conserv
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SERU

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APPLICANT: Li, Ping, TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRET APPLICATION NUMBER: US/10/437,963
CURRET APPLICATION NUMBER: US/10/437,963
CURRET FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 133945
LENGTH: 148
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_35767C.1.pep
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US-10-437-963-162813
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.9
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Oryza sativa
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42 LRAREPTPPL
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61 LSSLDPSPPL
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253125
LENGTH: 80
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Gaps
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US-10-424-599-253125
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70.0%; Pred. No. 45;
iive 1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.6
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Glycine max
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1 LKAMDPTP 8
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; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-720
                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PTC1
CURRENT FILING DATE: 2002-03-22
FRIOR APPLICATION NUMBER: 09/925,298
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
TENNYMER: PATENTING DATE: 2000-03-08
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Pred. No. 5.1e+02;
2; Mismatches 1; Indels
Sequence 720, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 77.87
Secondary 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 LRSQDPTPP 354
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ORGANISM: Homo sapiens
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US-10-767-701-51220
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NAME/KEY: SITE
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LENGTH: 75
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APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brabazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TURRENT APPLICANT: 105/10/437,963

CURRENT FILING DATE: 2003-05-14

SEQ ID NO 162816

SEQ ID NO 162816

TABETH APPLICANT: Library APPLICANT: Lib
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1 LOCATION: (50)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-288-720
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; Bedulication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION:
    PILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 1999-03-08
; PRIOR PILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 720
; LENGTH: 459
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 60.0°
Matches 6, Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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67 LSSLDPSPPL 76
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346 LRSQDPTPP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
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US-09-925-298-720
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Gaps

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Sequence 51220, Application US/10767701
; Sequence 51220, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
    APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(55535)B
; CURRENT PAPLICATION NUMBER: US/10/767,701
; CURRENT PILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3481-060-Q6-K1-D12.pep
US-10-767-701-51220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 138037, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
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RESULT 12 US-10-102-806-720

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APPLICANT: Zhou, Yihua
APPLICANT: Go, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Burkarov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138037
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## Publication No. US20050108791A1

## GENERAL INFORMATION:

## APPLICANT: Edgerton Michael D

## TITLE OF INVERTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

## TITLE OF INVERTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

## TITLE OF INVERTION: US/10/732,923

## CURRENT FILING DATE: 2003-12-04

## PRIOR PELICATION NUMBER: 10/310,154

## PRIOR PELICATION NUMBER: 10/310,154

## NUMBER OF SEQ ID NOS: 24149

## SEQ ID NO 1996

## LENGTH: 369

## LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.4%; Score 38; DB 17; Length 369; Best Local Similarity 75.0%; Pred. No. 5.9e+02; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_39462C.1.pep
US-10-437-963-138037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 26, 2005, 19:16:33 Job time : 71.6 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-732-923-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LKAMDPTPPL 10
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1 MPSQDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::||||
59 KAVEPTPP 66
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US-10-732-923-1996
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Run on:

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GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSED: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TASA
COUNTRY: USA
ZIP: 77401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLIANT OF A PROPERTY OF A PLING DATE:
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION S14
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PATTELEPHONE: 713-482-2961
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR MOLECULE TYPE: PEPTIDE IN SEQ ID HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-657-163A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 43223, A
Sequence 8760, Appli
Sequence 8760, Appli
                                                                                                   May 26, 2005, 18:29:58 ; Search time 22.8 Seconds (without alignments) 32.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 876(Sequence 42, Sequence 444, Sequence 232, Sequence 230, Sequence 230, Sequence 230, Sequence 667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-185-282-4
                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                  US-10-047-945-1
54
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Match Length DB
                                                                                                                                                                                                          1 LKAMDPTPPL 10
                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                          Perfect score:
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                                                                    OM protein
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Result

Sequence 5, Appli Sequence 12, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 11, Appli Sequence 47, Appli Sequence 2, Appli Sequence 2, Appli Sequence 32, Appli Sequence 33, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 32, Appli Sequence 31, Appli	
US-08-185-282-5 US-08-185-282-12 US-08-886-713-6 US-09-209-666-13 US-08-971-207-1 US-08-971-207-1 US-08-371-68-2 US-10-210-428-1 US-10-237-551-161 US-09-894-998A-47 US-08-998A-47 US-08-9113-825-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-2 US-08-37-210A-3 US-08-37-31-32 US-08-37-31-32 US-08-38-46-132-32 US-08-37-31-31	
648 648 648 648 648 657 825 825 826 1068 1078 1078 1078	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
22444444444444444444444444444444444444	

# ; Sequence 2, Application US/08657163A; Patent No. 5744449

ALIGNMENTS

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A

FWL-PAT-US-011

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Gaps

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Query Match
100.0%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels
             TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGARDER
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 45.09 MIRCOSA DK.

CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 7440
ZIP: 7440
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FUOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
RILING DATE: 2.2 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/310,340
FILING DATE: 2.2 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/059,387
FILING DATE: 10 MAY 1993
ATTOME JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGMENT TYPE: N
RIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PROTEIN IN SEQ ID NO: HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08657163A Patent No. 5744449
  JONAS PERALES, ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 713-482-296
TELEFAX: 713-663-7290
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                |||||||||||
1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                       1 LKAMDPTPPL 10
                                                                                                                                                                                                   3-8 NOV 1991
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                                                                                                                                                                                                                     US-08-310-340A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-657-163A-1
  AUTHORS:
                                                                                                                                                                          PAGES:
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08310340A
Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
TITLE OF INVENTION: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
                                                                                                               ö
                                                                                                               Gaps
                                                                                                               ö
                                                               Query Match 100.0%; Score 54; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0043; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OMPUTER: IBM COMPATIBLE
OMPRATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 2 SEPTEMBER 1994
CLASSIFICATION 1514
PRIOR APPLICATION 178.
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANIELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRACMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMTNO ACID
STRANDEDNESS: SINGLE
TOPOLGGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEPAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: TEXAS V
DEVELOPMENTAL STAGE: ADULT
  SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION
                                                                                                                                                        1 LKAMDPTPPL 10
                                                                                                                                                                                 ||||||||||
1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
    ; ORIGINAL SUI
US-08-657-163A-2
                                                                                                                                                                                                                                                                                        US-08-310-340A-1
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US-07-857-224B-42
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                   AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTENATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: LOTH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 54; DB 1; Length 15; 100.0%; Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.9%; Score 41; DB 4; Length 253; 100.0%; Pred. No. 20; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                             ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Xaa means any amino acid US-09-270-767-43223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WI
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: JONAS PERALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTPPL 10
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DATE: 3-8 NOV 1991

US-08-657-163A-1
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LENGTH: 253
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Gaps
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COUNTRY: Switzerland
ZIP: Gnote: this is an international post code) CH-8092
ZIP: Gnote: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION A376
PRIOR APPLICATION MATA: none
TELECOMMUNICATION INFORMATION:
TELEFROME: (International) 41 1 632 2830
TELEFRAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/07857224B

Patent No. 5958784

GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSED: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 4; Length 72; 75.0%; Pred. No. 11; 11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M: Saccharomyces cerevisiae
Protein kinase; Table 8 Column 48
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSEQ for Windows Version 4.0
SERVITH: 72
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AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
IITLE: The protein kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: Protein kinase PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RIMDPIPP 68
                                                                                                                                                                                                                                                                                                                                                                                            2 KAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                ORGANISM: Human
US-09-949-016-8760
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RESULT 9
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                                                                                                                                                                                                          APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Enian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & PAPA
   DB 2; Length 267;
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 15;
                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB.1996
CLASSIFICATION: 435
   Score 38; DB 2
Pred. No. 67;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                              Sequence 444, Application US/08602999A Patent No. 6184205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 444, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
   70.4%;
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LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7-
Query Match 70.4
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-602-999A-444
                                                                        1 LKAMDPTPPL 10
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31 LKVVDPTPEL 40
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5 RALPPTPPL 13
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US-09-500-124-444
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Sequence 232, Application US/09071035

Patent No. 6446043

GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Human Genome Sciences, Inc.
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                                      APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                               COMPUTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: END FO Compatible
COMPUTER: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: 170*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
QUILLIAM, Lawrenc
DER, Channing J.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60...
6. Conservative
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-09-500-124-444
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RALPPTPPL 13
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US-09-134-000C-6676
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Sequence 230, Application US/09071035

Sequence 230, Application US/09071035

Patent No. 6448043

Patent No. 6448043

TITLE OF INVENTION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9836992
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: PB3697;
TELEPRENCE/DOCKET NUMBER: PB3697;
TELEPRENCE/SIDOCKET NUMBER: PB3697;
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION FOR SEQ 10 NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: Amino acids

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INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KAMDPTPPL 10
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US-09-134-000C-6676

US-09-134-000C-6676

Sequence 6676, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTERCOCCUUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT FALING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PRIOR OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 6676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6583
LENGTH: 306
                                                Gaps
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DB 4; Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.5%; Score 37; DB 4; Length 291 66.7%; Pred. No. 1.1e+02; vative 1; Mismatches 2; Indels
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Score 37; DB Pred. No. 94; 1; Mismatches
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US-094489-039A-13655
'Sequence 13655, Application US/09489039A
'Patent:No. 6610836
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US-09-13-000C-6583
'Sequence 6583, Application US/09134000C
'Patent No. 6617156
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Query Match 68.5%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.
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Best Local Similarity 60...
6; Conservative
                                                                                          2 KAMDPTPPL 10
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Search completed: May 26, 2005, 19:08:37 Job time : 24 secs
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US-09-248-796A-20624

; Sequence 20624, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Wainstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPRENCE: 107196.132
; CURRENT APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; RIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20624
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMOMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMOMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF EXQ ID NOS: 14342
ERQ ID NO 13655
LENGTH: 323
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US-09-270-767-57016

US-09-270-767-57016

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 57016

LENGTH: 27
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.7%; Score 36; DB 4; Length 323; Best Local Similarity 77.8%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                        ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 77.8%;
Matches 7; Conservative
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                        Gaps
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Score 35; DB 4; Length 27; Pred. No. 18;
                        3; Mismatches
 64.8%;
55.6%;
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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19 LRPLDPSPP
                                               1 LKAMDPTPP
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2005, 18:26:23 ; Search time 23.7 Seconds (without alignments) 60.897 Million cell updates/sec Run on:

US-10-047-945-2 84 Title: Perfect score:

1 LKAMDPTPPLWIKTE 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SOFFIERS	
Result		Query				
No.	Score	Match	Length	DB :	OI .	Description
-	63	75.0	237	8	A42013	alpha-1-B-glycopro
7	46	54.8	1213	N	A54063	TATA-binding prote
m	44	52.4	695	~	E75099	hypothetical prote
4	44	52.4		~	T38769	hypothetical prote
2	44	52.4	1327	7	T09402	immunoglobulin-lik
9	43	51.2	341	~	AB0644	probable glycosyl
7	43	51.2	687	~	D86314	hypothetical prote
80	43	51.2	932	Н	A31898	hydroxymethylgluta
6	42	50.0	115	N	D71194	hypothetical prote
10	42	. 50.0	398	~	A81717	conserved hypothet
11	42	50.0	453	~	T04646	aspartate transami
12	42	50.0	564	Н	VHXPMV	major structural n
13	42	50.0	662	~	A29900	
14	41	48.8	151	Н	830146	ribosomal protein
15	41	48.8	339	~	JC5882	myocyte enhancer f
16	41	48.8	349	7	JC5881	myocyte enhancer f
17	41	48.8	411	~	AE2152	two-component sens
18	41	48.8	707	~	F86925	probable acyl-CoA
19	41	48.8	967	N	S58360	lantibiotic Pep5 b
20	41	48.8	975	~	T03004	exodeoxyribonuclea
21	41	48.8	1172	7	T00065	hypothetical prote
22	41	48.8	1559	~	T07757	probable DNA (cyto
23	40		97	N	S59888	
24	40	٠	205	~	S26854	micofilarial sheat
25	40	47.6	205	~	A40525	proline-rich sheat
56	40	٠	209	7	B40049	virC-region hypoth
27	40	47.6	209	7	T43565	type III secretion
28	40	47.6	210	7	S21428	hypothetical prote
53	40	47.6	225	~	C70045	two-component resp

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77	256	84	167	146	104	808	187	114	25	552	986	928	SPN	157	110
F6997	H72626	A970	C83867	D86446	T024	8652	D863	E706	T450	F87552	A572	AD15	WMBE	T235	8310
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231	309	337	406	422	260	609	1184	1215	3570	365	631	242	256	258	268
			ဖ	७.	9.	9.	9.6	7.6	9.1	7.0	7.0	5.4	5.4	6.4	6.4
	9.7	٦.	ζ.	7											
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## ALIGNMENTS

RESULT 1 A42013 31-bhs.1-B-cluconrotein - North American onogenum (fracmente
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C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004

C;Accession: A42013
R;Catanese, J.J.; Krese, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum A;Teference number: A42013; MUID:92118834; PMID:1731898
A;Accession: A42013
A;Accession: A42013
A;Accession: A42013
A;Accession: A2013
A;Accession:

Gaps .. 0 Length 237; Score 63; DB 2; Length 237 Pred. No. 0.0095; 1; Mismatches 2; Indels Query Match 75.0%; Best Local Similarity 80.0%; Matches 12; Conservative

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1 LKAMDPTPPLWIKTE 15 ð g

TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

CyAccession: A54063
R;Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.
Science 264, 933-941, 1994
A;Title: Drosophila TAF-II 150: Bimilarity to yeast gene TSM-1 and specific binding to c.
A;Reference number: A54063; MUID:94233377; PMID:8178153
A;Reference number: A54063 MUID:94233377; PMID:8178153
A;Retus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1213 <VER>
A;Residues: 1-1213 <VER>
A;Cross-references: UNIPROT:Q24325; GB:X79243; NID:9541664; FIDN:CAA55830.1; PID:9541665

C;Genetics:

A;Gene: FlyBase:Taf150 A;Cross-references: FlyBase:FBgn0011836

Gaps ö Length 1213; 4; Indels ilarity 53.3%; Score 46; DB 2; larity 53.3%; Pred. No. 32; Conservative 3; Mismatches 4 Query Match Best Local Similarity Matches 8; Conserva

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620 LSAMDDSPVLWIRLD 634 1 LKAMDPTPPLWIKTE 15 ઠે g

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217 RAIDPRPASGSPYWLKT 233
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Best Local Similarity 63.6
Matches 7; Conservative
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25 MDPQPELWIES
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Matches 8; Conserv
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A;Molecule type: DNA
                                                                                                                                                                                                      A, Map position: Xq25
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C;Species: Schizosaccharowyces pombe
C;Species: Schizosaccharowyces pombe
C;Date: 20-oct.2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004
C;Accession: T38769; T38072
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
R;Gentles to the EMBL Data Library, January 1996
A;Recence number: Z21810
A;Recession: T38769
A;Molecule type: DNA
A;Resperimental source: strain 972h-; cosmid c3H8
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Experimental source: strain 972h-; cosmid c3H8
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21767
A;Reference number: Z21767
A;Reference number: Z21767
A;Reference number: Z21767
A;Residues: 90-777 cCON>
A;Residues: 90-777 cCON>
A;Residues: 90-777 cCON>
A;Residues: 90-777 cCON>
A;Residues: BMBL:Z70690; NID:g1256511; PIDN:CAA94619.1; PID:g3859771; GSPDB:GNOG A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Genetics: Space: SPAC3H8.11; SPDB:SPAC1F3.01
A;Mon conficiental source: strain 972h-; cosmid c1F3
A;Mon conficiented conficie
                                                                                       C)Accession: E7509
R) Anonymous, Genoscope
Bubmitted to the EMBL Data Library, July 1999
A) Bescription: Eyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A7501
A;Accession: E7509
A;Accession: E7509
A;Accession: E7509
A;Accession: E7509
A;Restius: pre-liminary
A;Molecule type: DNA
A;Restius: pre-ferences: UNIPROT:Q9UZG1; GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB5009
C;Genetics:
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                                  Species: Pyrococcus abyssi
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Accession: T09402
R;Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger,
Pothetical protein PAB1590 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2; Length 695;
Pred. No. 36;
3; Mismatches 2; Indels
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54.5%;
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212 SVDETEPIWVSTE 224
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Best Local Similarity 46.2<sup>3</sup>
Matches 6; Conservative
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561 ANDPKPPMWLE 571
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Best Local Similarity
Matches 6; Conserv
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A,Gene: PAB1590
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A;Molecule type: mRNA
Kseidues: 1-1327 <MAZ>
A;Cross.references: UNIPROT:015070; EMBL:AF034198; NID:92645889; PIDN:AAC52057.1; PID:92.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disposable glycosyl hydrolase STY1249 [imported] - Salmonella enterica subsp. enterica ser C; Species: Salmonella enterica subsp. enterica serovar Typhi C; Date: Salmonella enterica subsp. enterica serovar Typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: AB0644

E; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 411, 848-852, 2001

A; Aththors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov. A; Reference number: AB0502; MUID:21534947; PMID:11677608
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.X.; Liu, Z.X.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
Genomics 48, 157-162, 1998
A;Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.
A;Reference number: Z16665; MUID:98190514; PMID:9521868
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                             A, Accession: T09402
A, Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 75;
2; Mismatches
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Pred. No. 24;
3; Mismatches
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Gaps

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 «TET>
A;Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-May-1999 #sequence revision 21-May-1999 #text_change 09-Jul-2004
C;Cacession: T04646; S56657; Sq1490
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana N;Alternate names: aspartate aminotransferase; protein F10N7.200
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A;Note: F10N7.200
                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Chlamydia muridarum, Chlamydia trachomatis Mořn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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A;Cross-references: EMBL:X81026; NID:9531554; PIDN:CAA56932.1; PID:9531555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: Chlamydia trachomatis hypothetical protein CT036
                                      Length 115;
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                                      2,
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                                      Score 42; DB Pred. No. 10; 2; Mismatches
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                                                                                                 2;
                                      50.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                        Conservative
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                                                                                                                                                                       12
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      Query Match
Best Local Similarity
                                                                                                                                                                       4 MDPTPPLWI
                                                                                                                                                                                                                                      89 ISPSPPLWI
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Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A81717
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A;Genome: nuclear
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431898
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrot C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A31898; A28367
C;Accession: A31898; A28367
J. Biol. Chem. 263, 18411-18418, 1988
A;Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deductarence number: A31898; MUID:89054023; PMID:3192541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Note: the authors translated the codon GGA for residue 805 as Glu
R.Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
Biol. Chem. 263, 2513-2517, 1988
A;Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev
A;Reference number: A28367; MUID:88115403; PMID:3276692
A;Rocession: A28367
A;Molecule type: mRNA
A;Residues: 689-735 <WO2>
C;Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t
C;Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C;Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N
F;279,850,886,930/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A, Cross-references: UNIPROT: Q9LMT8; GB: AE005172; NID: 99665069; PIDN: AAF97271.1; GSPDB: GN
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A;Note: the authors rearranged portions of the coding region in Figure 2, and the above submitted to GenBank
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Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PH1828 - Pyrococcus horikoshii
C;Species: D71034
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, S5-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: D71194
A;Residues: D1194
A;Residues: 1-115 <KAWA>
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                                                              A;Map position: 1
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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                                                                                                                                                                                                       DB 2; Length 687;
52;
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Pred. No. 73;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                   51.2%; Score 43; DB ilarity 46.7%; Pred. No. 52; Conservative 3; Mismatches
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298 KKIDPTMPLW 307
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Best Local Similarity
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-932 <WOO>
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Search completed: May 26, 2005, 18:44:46 Job time : 26.7 secs
  ribosomal protein S13, cytosolic - maize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TPPLWIKT 14
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: Mef2b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fasciclin I precursor - American bird grasshopper C;Species: Schistocerca americana (American bird grasshopper)
C;Species: Schistocerca americana (American bird grasshopper)
C;Date: 22-Aug-1988 #sequence revision 22-Aug-1988 #text_change 09-Jul-2004
C;Accession: A29900; A31817
R;Zinn, K.; McAllister, L.; Goodman, C.S.
Cell 53, 577-587, 1988
A;Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Drc A;Reference number: A29900; MUID:88223351; PMID:3370670
A;Accession: A29900
A;Accession: A29900
A;Reference number: A29900; MUID:8822351; PMID:3370670
A;Reference number: A29900; MUID:8822351; PMID:3370670
A;Accession: A29900
A;Residues: 1-662 <ZIN>
A;Cross-references: UNIPROT:PI0675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
B;Snow, P. M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.; Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988
A;Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in the A;Reference number: A34202; MUID:88276943; PMID:2839842
A;Accession: A31817
A;Molecule type: mRNA
A;Residues: 22-42 <<300>
A;Accession: A31817
A;Molecule type: mRNA
A;Residues: 25-42 <<300>
A;Accession: A31817
A;Molecule type: mRNA
A;Residues: 25-42 <<300>
A;Accession: A31817
                                                                                                                                                                                                                                                                                                 Major structural nucleoprotein - Machupo virus
NiAlternate names: nucleocapsid protein
Cipacte: Martenames: nucleocapsid protein
Cipacte: Machupo virus
Cipate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
Cipate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
Cipate: 31-Mar-1994
Cipate: Martifiths, C:; Wilson, S.M.; Clegg, J.C.S.
Striffiths, C:; Wilson, S.M.; Clegg, J.C.S.
Striffiths, C:; Wilson, S.M.; Clegg, J.C.S.
Striffiths, C:; Wilson, S.M.; Clegg, J.C.S.
A.Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship will A.Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship will A.Molecule type: genomic RNA
A.Molecule type: genomic RNA
A.Molecule type: Genomic RNA
A.Molecule type: Genomic RNA
A.Kosidues: 1-564 <GRI>
A.Kosidues: 1-564 <GRI>
C.Genetics:
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Pred. No. 72;
1; Mismatches 4; Indels
  DB 2; Length 453;
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                                                        2; Indels
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                                                        2; Mismatches
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                            47;
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C;Superfamily: arenavirus major nucleoprotein
C;Keywords: nucleocapsid; nucleoprotein
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  Score 42;
Pred. No.
  50.0%;
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Best Local Similarity 58.3
Matches 7; Conservative
Query Match 50.0
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                             238 IDPTPEQWVK 247
                                                                                             4 MDPTPPLWIK 13
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Matches 7; Conserv
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RESULT 14

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C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Jacesion: D: 7 Gigot, C:; Philipps, G.
Plant Mol. Biol. 21, 701-704, 1993
PATILL: CDNA muclectide sequence and expression of a maize cytoplasmic ribosomal protein A;Reference number: S30146; MUID:93192530; PMID:8448368
                                                                                                                                                                                                                                                                                                                                                                                                                                PID:92880
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myocyte enhancer factor 2B-2 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11.Mar-1998 #sequence_revision 11-Mar-1998 #text_change 09-Jul-2004
C;Accession: 4C5882
R;Morisaki, T.; Sermsuvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki, H.; J. Biochem. 122, 939-946, 1997
J. Biochem. 122, 939-946, 1997
A;Fitle: Mouse Mef2b gene: Unique member of MEF2 gene family.
A;Reference number: 4C5881; MUID:98104045; PMID:9443808
A;Accession: JC5882
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C;Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.
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A,Reaidues: 1-151 <-700A
A,Reaidues: 1-151 <-700A
A,Cross-references: UNIPROT:Q05761; EMBL:X62455; NID:9288058; PIDN:CAA44111.1; PID:93
C,Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
C,Reywords: protein hissynthesis; ribosome
C,2-151/Product: ribosomal protein S13 #status predicted <MAT>
F;2-151/Product: ribosomal protein S13 #status predicted <MAT>
F;2-151/Product: ribosomal protein S15 homology <ES15>
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Pred. No. 50;
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  DM43 DII
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Q8fnb0
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Q7qe48
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Q7yqj7 |
Q18150
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Q8bxk6
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Q8hz73
Q8hz73
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                            1612378 seqs, 512079187 residues
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DM43 DIDMR
08H275
08H275
08H274
08HXX5
08HXS3
073ZB2
07MTQ9
07MTQ9
07MTQ9
07QENB0
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RRPL_AHSV9
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Q7YQJ7
Q18150
Q9NV61
Q8N6C5
Q8BXK6
Q8HZ72
Q8HZ73
Q9LT32
                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                           1 LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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84
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Match Length
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777
1305
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856
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Maximum DB seq
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No
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                          082tel nitrosconora
0946h8 oryza sativ
064cus oryza sativ
07vziz bordetella
07w5y0 bordetella
07w5y0 bordetella
08z7i6 salmonella
08z76 salmonella
08wm74 rhizobium s
094467 arabidopsis
072c38 desulfovibr
   sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
"Isolation and partial characterization of an anti-bothropic complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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Pred. No. 3.1e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1947 MW; CB55FB40E73B2A2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment)
Didelphis marsupialis (Southern opossum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the serum of South American Didelphidae.";
Toxicon 32:1237-1249(1994).
SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
26-UJL-2004 (Rel. 44, Last annotation update)
Venom metalloproteinase inhibitor DM43.
                                                                                                                                                                                                                                                                                                                                     17 AA.
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                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                             OGERUS
Q7VZ12
Q7W5Y0
Q7WGN4
NAGZ_SALTI
NAGZ_SALTY
                                 Q82TE1
Q946H8
                                                                                                                                                                          Q846T8
Q944S7
                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
NCBI_TaxID=9268;
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Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
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TISSUE=Liver;
                                                                                                   SEQUENCE FROM N.A.
                            NCBI_TaxID=9267;
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01-OCT-2002 (
01-MAR-2004 (
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Q8MIS3;
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Jodelphis marsujalis virginiana (North American opossum).

Bukaryota Metazoa; Chordeta; Craniara; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North-American opossum).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
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                                                                                    NOISERGELI.
-!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
N-glycosylated.
SPECTROMETRY: MW-42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 291;
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Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY131000; AAN06911.1; --
HSSP; O76036; 10LL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17A496227E69A65B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84; DB 1; Pred. No. 5.9e-05;
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100.0%;
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 100...
Best Local Similarity 100...
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                                                                      NOTE=Ref.1
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NON TER
SEQUENCE
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Q8HZ75;
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Q8HZ75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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       NO COCCOS EL PACA COC
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Gaps
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venom metalloproteinase inhibitor DM43b.
69D55F54486D35A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Didelphis marsupialis (Southern opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Didelphlmorphia; Didelphidae, Didelphis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
TISSUE-Liver;
Martinez M.B., Pierce J.R.;
Martinez M.B., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY1310011, AAN06912.1; -.
HSSP; Q8NHL6; 1GOX.
InterPro; IPR007110; Ig.
InterPro; PR007110; Ig-like.
Pfam; PF00047; 1g; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                            291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update
Venom metalloproteinase inhibitor DM43b precursor.
                                                                                                                                                                                                                                                                            Match 89.3%; Score 75; DB 2; Local Similarity 93.3%; Pred. No. 0.0015; es 14; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No. 0.12;
1; Mismatches
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CHAIN 24 314 Vu
SEQUENCE 314 AA; 34604 MW;
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80.0%;
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(TrEMBLrel. 22, I
(TrEMBLrel. 26, I
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                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTPRLWIKTE 15
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE;
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Best Local Similarity 80.0
Matches 12; Conservative
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Perales J

SEQUENCE

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MEDLIANS 228 867; PubMed=12949112;

MEDLIANS 228 867; PubMed=12949112;

MEDLIANS 228 867; PubMed=12949112;

MEDLIANS 258 867; PubMed=12949112;

MEDLIANS 258 867; Melson R.D., DeBOY R.T., Paulsen I.T., Fouts D.E.,

Reisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,

Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,

A Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

M. Dewhirst F.E., Fraser C.M.; Melson W.C., Mason T.M., Tallon L., Gray J.,

A Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

M. Dewhirst F.E., Fraser C.M.;

"Complete genome sequence of the oral pathogenic bacterium

Porphyromonas gingivalis strain W83.";

"Gonglete genome sequence of the oral pathogenic bacterium

"TGR; PG1887;

"Ap66871.1;

"Ap66871.1;

"Melson Melson Mel
                                                                                                                                                                                                                                                 Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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                                                                                                                                                      01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                   344 AA.
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                                                                                                                                 Created)
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EMBL; AP005221; BAC19045.1; -.
                                                                                                                                                                                                      Rhodanese-like domain protein.
OrderedLocusNames=PG1887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 LSACDPNRPIWVESE 213
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OrderedLocusNames=CE2235;
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                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=837;
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                                                                                                                                    01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=W83
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                                                                              Q7MTQ9
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08FNB0
                                 RESULT 8
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Venom myotoxin inhibitor DM64 precursor.
Didelphis marsupialis (Southern opossum)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                   "Punctional analysis of DM64, an antimyotoxic protein with
immunoglobulin-like structure from Didelphis marsupialis serum.";
Eur. J. Biochem. 269:6052-6062(2002).
                                                                                                                                                                                                                                                    Rocha S.L., Lomonte B., Neves-Ferreira A.G., Trugilho M.R.,
Junqueira-De-Azevedo Id I., Ho P.L., Domont G.B., Gutierrez J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rocha S.L.G., Neves-Ferreira A.G.C., Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AX7078394 AAL82794.1; -
HSSP; P24071; 10VZ.
InterPro; IPR003599; Ig.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017233; AAS04008.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium paratuberculósis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            venom myotoxin inhibitor DM64.
0446529A6CBA63B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                             MEDLINE=22361219; PubMed=12473101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55975 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 3.
PROSITE; PSS0835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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146 LAALDPRPPLW 156
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504
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Liver;
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Matches 10; Conserv
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                                                                                                                                                                             FROM N.A.
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SEQUENCE Query Match

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CHAIN

Q73ZB2

RESULT 7
073282
AC 073282
DT 05-JI
DT 0

Signal

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                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
       Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
57.1%; Score 48; DB 2; 46.7%; Pred. No. 30;
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Query Match

Matches

Y4VJ_RHISN

Matches

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MEDINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., Stories S.E., Li P.W., Hoskins R.A., Galle R.F., Stories S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Abardon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfelifer B.D., Ann K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Abards S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Downes M., Dugan-Rocha S., Pleischmann W., Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                             AgCP7225 (Fragment).
Name-agCG51396; ORFNames-ENSANGG0000014288;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                         Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Contains 2 C2 domains.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=E23; ORFNames=CG3327;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8D8F CRC64;
(TrEMBLrel. 26, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016020; C:membrane; IEA.
GO; GO:0008021; C:synaptic vesicle; IEA.
GO; GO:0008215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001149; Alatroxin_recept.
InterPro; IPR008973; C2_CalB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
EMBL; AAAB01008848; EAA07048.1; -.
HSSP; P21707; 1K5W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50004; C2_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00168; C2; 2. -
PRINTS; PR00360; C2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::|:||| |:|
294 IRALDPTNPIW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LKAMDPTPPLW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                   01-MAR-2004
                                                                                                                                                                                                                                                                                                                   STRAIN-PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VQP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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      ઠે
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                                                                                                                              ö
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
BEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beginning.";
Genome Res. 6:590-600(1996).
-!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-279 FROM N.A. MEDLINE=96389014; MEDLINE=96389014; PubMed=8796346; Freiberg C., Perret X., Broughton W.J., Rosenthal A.; Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable 'sequenase': a
                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Monooxygenase; Oxidoreductase; Plasmid. SEQUENCE 351 AA; 39158 MW; 866BDE3BBA40C8BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid sym pNGR234a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.0%; Score 47; DB 1; Length 351; 77.8%; Pred. No. 44;
                                                             Score 47; DB 2; Length 51;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                              Indels
   759F3C5BDCCE414A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Hypothetical 39.2 kDa protein y4vJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             351 AA
                                                                                                                          5; Mismatches
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InterPro; IPR002103; Bac_luciferase.
InterPro; IPR011251; Luciferase like.
Pfam; PF00296; Bac_luciferase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain NGR234).
   51 AA; 5686 MW;
                                                             56.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 387:394-401(1997).
                                                                                                                          6; Conservative
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hes 7; Conservative
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                                                                                                                                                                                        3 AMDPTPPLWIKT 14
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21 SLDPTPRVWVET 32
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 PrPPIWIAT 175
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                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=y4vJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium sp.
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Q53218;
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   SEQUENCE
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Q7QE48;
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Matches

RESULT 11 Q70E48

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Gaps

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Length 370; 1; Indels S

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Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., A Harris N.L., Harvarby D., Helman T.J., Hernandez J.R., Houck J., Howland T.J., Mein M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Armel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.C., McLeed M.P., Mopherson D., Merkulov G., Milahina N.V., Mobarry C., Morris J., Mosherefi A., March C., Michon K., March D.R., Pacleb D.L., Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun S., Wang Z.Y., Wassarman D.A., Weinsteck G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Walliams S.M., Weedes E.W., Rubin G.M., Venter J.C.; The Gonome sequence of Enosophila melanogaster.";

The genome sequence of Enosophila melanogaster.";
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0045262; F:ATPase activity, coupled to transmembrane m. . .; IEA.

GO; GO:0000166; F:Atplectide binding; IEA.

GO; GO:0000810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22126065; PubMed=12537568,
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirsks R., Tabor P.E., Wan K., Staplecton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AE003580; AAF51122.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3enome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDILARS-21056005 PubMed=10731132; DOI=10.1126/science.287.5461.2185;

Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ambourner M., Henderson S.N.,

Barandon R.C., Rogares Y.H., Blazei R.G., Champe M., Fefifer B.D.,

RA Barandon R.C., Rogares Y.H., Blazei R.G., Champe M., Fefifer B.D.,

RA Barandon R.C., Rogares Y.H., Blazei R.G., Champe M., Fefifer B.D.,

RA Ballew R.M., Benos P.V., Berman B.P., Blandari D., Bolshakov S.,

RA Ballew R.M., Cavales B.D., Butler H., Cadieu E., Center A., Chandra I.,

Ra Ballew R.M., Cavales B.D., Butler H., Cadieu E., Center A., Chandra I.,

Ra Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ra Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ra Butles K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ra Butles K., Doup L.E., Downes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

Burdin K., Doup L.E., Downes M., Dugan-Rochs S., Dunkov B.C., Dunn P.,

Butlis K., Gong F., Gorrell J.H., Gu Z., Ganp W., Harris M.,

Randolek A., Howland T.G., Wei M.H., Ibeyam C.,

Ra Harris N.L., Harvey D., Heiman T.G., Wei M.H., Ibeyam C.,

Ra Harris N.L., Harvey D., Marphy B., Wairy D.M., Nelson D.,

Randock K., Mattel B., McIncohn T.C., Morted G., Mosterio J., Morted G., Milahina N.V., Mobarry C., Morris G., Moster G., Morted G., Milahina N.V., Mobarry C., Morris G., Moster M., Mount S.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,

Rander D.R., Nelson K.A., Nixon K., Nuskern D.R., Pachel P., Shen H.,

Rander R., Spradling A.C., Stapleton M., Stupsk M. P., Nang S., Yao Q.A., Ye J.,

Rander R., Spradling A.C., Stapleton M., Stupsk M. P., Nang S., Yao Q.A., Ye J.,

Rander R., Spradling A.C., Stapleton M., Stupsk M. Sheng S., Rand B.,

Rander R., Mores E., Represe M., Rubier C., Wu D., Yang S., Yao Q.A., Ye W.,

Rander R., Morre E., Wasserman D.A., Weiller E., Wasserman D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=E23; ORFNames=CG3327;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Meoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                 Length 634;
                                                                                                                                                                               54.8%; Score 46; DB 2; Length 634
57.1%; Pred. No. 1.2e+02;
ive 2; Mismatches 4; Indels
                                                                                                                                        634 AA; 72223 MW; A9D0900DCDB04B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   854 AA
                                                                           PROSITE; PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
                 InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC tran; 1.
SMART; SM00382; AAA; 1.
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InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                           594 LKAQNSTSPLWLNT 607
                                                                                                                                                                                                                                                                  1 LKAMDPTPPLWIKT 14
                                                                                                                                                                                                       Local Similarity 57.1 tes 8; Conservative
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01-MAY-2000 (
01-OCT-2002 (
                                                                                                                  ATP-binding.
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                                                                                                                                        SEQUENCE
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Bernos P.V., Bernan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                Drosophija melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856 AA; 95080 MW; BAAE8964A5D806D6 CRC64;
                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, coupled
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
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InterPro; IPR003439; ABC transporter.
PF000, PF00005; ABC tran; 1.
SMART; SM00382; AAA; 1.
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816 LKAQNSTSPLWLNT 829
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Name=E23; ORFNames=CG3327;
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                          01-MAR-2001
01-MAR-2001
01-MAR-2004
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                                              MEDLINE-22456065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Calniker S.E., Wheeler D.A., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.W., Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fribe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AE003580; AAF51121.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                     melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Flyase, PBgn0020445, E23.

GO; GO:0016020; C:membrane; IEA.

GO; GO:00042624; F:ATP binding; IEA.

GO; GO:00042626; F:ATPase activity, coupled to

GO; GO:0000166; F:ATPase activity, coupled to

GO; GO:0000166; F:ATRANGPOTE; IEA.

INTERPO: IPR003593; AAA ATPase.

InterPro: IPR003439; ABC_transporter.

Pfam; PP000065, ABC_tran; 1.

PRODOM: PD0000065, ABC_tran; 1.
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
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MEDLINE=22426070; PubMed=12537573;
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814 LKAQNSTSPLWLNT 827
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

A dodek A., Gong F., Gorgell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heinan T.J., Wei M.H., Ibegwam C.,

A dalai M., Kalush F., Karpen G.H., Ke Z., Kanison J.A., Ketchum K.A.,

A lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

A lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Mattei B.L., McIntosh T.C., Morris J., Moshrefi A.,

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Shu B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genomics perspective.";
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     F:ATPase activity, coupled to transmembrane m. . .; IEA F:nucleotide binding; IEA.
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                                                                                                                                                                                         1017 AA; 112351 MW; D3F096E05E6EC76F CRC64;
GO; GO:0042626; F:ATPase activity, coupled GO; GO:0000166; F:nucleotide binding; IEA GO; GO:0006810; P:transport; IEA.

InterPro; IPR003593; AAA, ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR011051; RmlC_like cupin.
Probom; PD0000066; ABC_transporter; I.
PROSITE; SM00382; AAAA; I.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
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May 26, 2005, 18:17:22 ; Search time 129 Seconds (without alignments) 44.972 Million cell updates/sec Run on:

1 LKAMDPTPPLWIKTE 15 US-10-047-945-2 84 Title: Perfect score: Sequence:

Scoring table:

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2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp19908:* geneseqp20008:* geneseqp20018:* geneseqp20028:* geneseqp2003as:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

#### SUMMARIES

u O:	N-termina	N-terminu	Synthetic	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic		Human NOV	Neisseria	Neisseria	Drosophil	TATA-bind	Drosophil	TATA-bind	Drosophil	Enterococ	Neisseria	Bovine ph	Peptide #	Human bon	Human bra	Zеа шаув	Zea maye
Description	Aaw11575	Aaw53841	Abb80223	Abb80225	Abb80226	Aaw53843	Abb80222	Abb80227	Abg18144	Abr54218	Aay74721	Aay74718	Abb59797	Aar56496	Aaw06086	Aaw25029	Abb62618	Adh88053	Aay74720	Abu62528	Abb42105	Aam75798	Aam62985	Aag54516	A2054515
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ID	AAW11575	AAW53841	ABB80223	ABB80225	ABB80226	AAW53843	ABB80222	ABB80227	ABG18144	ABR54218	AAY74721	AAY74718	ABB59797	AAR56496	AAW06086	AAW25029	ABB62618	ADH88053	AAY74720	ABU62528	ABB42105	AAM75798	AAM62985	AAG54516	AAG54515
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% Query Match	100.0	100.0	100.0	82.1	77.4	64.3	64.3	59.5	26.0	56.0	54.8	54.8	54.8	54.8	54.8	54.8	54.8	53.6	53.6	53.6	52.4	52.4	52.4	52.4	52 4
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AAG54605 AAG54604 AAG10737 AAB93318 ABB22890 AAB90651 ADP18673 AAU32796 ABB80228 AAU32796 ABU42550 ABU42550 ABU47244 ABU47244 ABU47244 ABU47244 ABU47970 AAM79784	AAG27882 AAG27881
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# ALIGNMENTS

Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite. N-terminal peptide from lethal toxin neutralising factor. AAW11575 standard; peptide; 15 AA. 93US-00058387. 94US-00310340. (revised)
(first entry) Didelphis virginiana. Lipps FW, Lipps BV; WPI; 1997-011287/01. (LIPP/) LIPPS B V. (LIPP/) LIPPS F W. 22-SEP-1994; 10-MAY-1993; 25-MAR-2003 20-MAR-1997 US5576297-A. 19-NOV-1996. AAW11575; AAW11575 

Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.

Claim 7; Col 9; 9pp; English.

The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (ITNF). The use of purified LINF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence of significant neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LINF and the 15mer peptide against venom from snakes of the families Crotalidae, Elaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                      ABB80223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2002; 2002US-00047945.
                                                                                                                           06-NOV-2003 (first entry)
                                                                                                                                                               Synthetic LTNF, LT-15
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                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                        ABB80223;
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                  RESULT 3
                                     ABB80223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) molety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of some bites, recorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                             LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
                                                                         Gaps
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                                   Length 15;
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                               100.0%; Score 84; DB 2; L
100.0%; Pred. No. 2.1e-06;
iive 0; Mismatches 0;
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94US-00310340.
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                                                                                                        1 LKAMDPTPPLWIKTE 15
                                                                                                                                      LKAMDPTPPLWIKTE 15
                                                                                                                                                                                                                                                                                                                                             N-terminus of opossum LTNF.
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Didelphis virginiana.
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К.
                                                  Local Similarity
les 15; Conserv
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Sequence 15 AA;
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(LIPP/) LIPPS
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                                   Query Match
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                                                                       Matches
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (19E), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins
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Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                        Claim 3; Page 3; 24pp; English.
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RESULT 4 ABB80225

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1 LKAMDPTPPLWIKTE 15 

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15; Conservative

Best Local Similarity Matches 15; Conserv

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; 19B; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;

Synthetic LTNF, LT-11.

14-JAN-2003; 2003WO-US001044. 14-JAN-2002; 2002US-00047945

WO2003060471-A2.

24-JUL-2003.

saliva; ELISA

Synthetic.

Lipps BV, Lipps FW; WPI; 2003-636703/60.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (MCF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, attoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, c.g. Addison's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of the care of the collection is relatively non-invasive when compared to blood collection of the care of the collection is relatively non-invasive when compared to blood collection of the care of the collection of the care of the ca
                                                                                                                                                                                                                                    Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
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serum requires a more complicated sandwich type ELISA
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ABB80225 standard; peptide; 12
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                                                                                                                  (first entry)
                                                                                                                                                                                 Synthetic LTNF, LT-12
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                                                                                                                     06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                            ABB80225;
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e.g.

Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a

Claim 7; Page 4; 24pp; English.

patient.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva cantering an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires
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serum requires a more complicated sandwich type ELISA
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LKAMDPTPPLW
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Local Similarity

Query Match

ABB80226 standard; peptide; 11 AA

ABB80226;

ABB80226 ID ABB XX AC ABB

82.1%; Score 69; DB 7; Length 12; 100.0%; Pred. No. 0.0004;

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (IgE), nerve growth factor (MCF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and traing conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (BLISA) on a saliva canderine. Saliva can be centrifuged immediately, whereas blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple BLISA test, whereas an assay of proteins from serum requires a more complicated sandwich type BLISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 3; 24pp; English.
                                                                                                                                        14-JAN-2003; 2003WO-US001044
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                            WO2003060471-A2
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                                                                                  24-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  %XXCCCCCCCCCCCCX8X4444X4X4X4X4X4X4X4X4XAXAXAXAXAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) molety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 10gE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sionarmanes syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 54; DB 2; Length 10; 100.0%; Pred. No. 0.078; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB80222 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Col 11; 11pp; English.
                                                                                                                                     histamine reaction treatment
                                                                                                                                                                                                                                                                                                                                                       96US-00657163
                                                                                                                                                                                                                                                                                                                                                                                                             93US-00058387
94US-00310340
N-terminus of opossum LTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 64.3
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic LTNF, LT-10.
                                                                                                                                                                                        Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-271108/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                          03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1994;
                                                                                                                                                                                                                                              US5744449-A
                                                                                                                                                                                                                                                                                                    28-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB80222;
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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                         ABB80227 standard; peptide; 9 AA.
                                                                                                                                                       06-NOV-2003 (first entry)
|||||||||||
1 LKAMDPTPPL 10
                                                                                                                                                                                    Synthetic LTNF, LT-9.
                                                                                                                                                                                                                                                                                                                                                            WO2003060471-A2
                                                                                                                                                                                                                                                                                                 saliva; ELISA.
                                                                                                                                                                                                                                                                                                                             Synthetic.
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saliva; ELISA

RESULT 7 ABB80222

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Synthetic

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Gaps

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64.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.078; ive 0; Mismatches 0; Indels

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(HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR54218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR54218
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                        The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (198), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum 19E levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatodid arthritis, Sjogran's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifuged immediately, whereas blood requires can be assayed by a simple ELISA, test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                             Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.5%; Score 50; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #18135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG18144 standard; protein; 303 AA.
                                                                                                                                                                                                       Claim 7; Page 4; 24pp; English.
                      14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                           14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKAMDPTPP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                   Lipps BV, Lipps FW;
                                                                                                                         WPI; 2003-636703/60
                                                                 (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002
24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
                                                                                                                                                                                 patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders conjuppited and polynucleotide sequences halological activity. The polypeptide and polynucleotide sequences have applications in dispussion of dispussion of dispussion of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and canno acid sequences. ABGOOID-ABG30377 represent novel human dispussion patent did not appear in the printed specification, but was obtained in the with the printed specification, but was obtained in the printed partners and produces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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Pred. No. 35;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 48503; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV21a protein SEQ ID NO:104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR54218 standard; protein; 531 AA.
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KAMDPTPPLWIKTE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS82331.
Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 303 AA;
                                                                                                                                                                                                                                                                                                                                                                                   biodiversity.
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Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
Kakuda K, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
Malyankar UM, Miller CE, Oot ET, Padigaru M, Patturajan M;
Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
Zerhusen BD, Zhong M;
                                                                                        2001US-0322636P.
2001US-0322818P.
2001US-0322817P.
2001US-0323819P.
2001US-0323631P.
2001US-0323631P.
                                                                                                                                                        2001US-0324969P.
2001US-0325091P.
2001US-0324990P.
2001US-0341144P.
                                                                                                                                                                                             2002US-0359599P.
2002US-0361663P.
2002US-0377908P.
2002US-0381483P.
                                                              2001US-0318120P.
2001US-0318184P.
2001US-0318430P.
                                                                                                                                                                                                                                  29-MAY-2002; 2002US-0383863P
02-JUL-2002; 2002US-039332P
                                             09-SEP-2002; 2002WO-US028538
                                                                                                                                                                                                                                                                       06-SEP-2002; 2002US-00236417
                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-313241/30.
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACC62287.
        WO2003023001-A2.
                                                                                                                                                         25-SEP-2001;
                                                                                                                                                                   25-SEP-2001;
                                                                                                                                                                           26-SEP-2001;
14-DEC-2001;
                                                                                                                                                 20-SEP-2001;
                                                                                                                                                                                             26-FEB-2002;
                                                                                                                                                                                                       05-MAR-2002;
                                                                                                                                                                                                               03-MAY-2002;
                                                                                                                                                                                                                         17-MAY-2002;
                           20-MAR-2003
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The present invention describes isolated human NOVX proteins, where X is

1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
ABR54167 to ABR54276. NOVX sequences have antiatheroscolerotic, cardiant,
hypotennsive, dermatological, anorectic, immunosuppressive, cytostatic,
antidabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antidatestic, metabolic, immunomodulator, neuroprotective, noctropic,
antiparkinsonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with a NOVX protein in humans and for treating a syndrome
associated with the human disease. NOVX nucleic acids, proteins and
antibodies can be used in the treatment and diagnosis of cardiomyopathy,
atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
congenital adrenal hyperplania, prostate cancer, fertility, haemophilia,
hyperclassin, lymphoma, uterus cancer, fertility, haemophilia,
infectious disease, anorexia, cancer-associated cachexia, cancer,
haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
Alzheimer's disease, parkinson's disease, immune disorders,
haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
ACC62346 to ACC62465 represent PCR primers and probes for human NOVX Novel human proteins and nucleic acid encoding the proteins, useful for diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders. Claim 1; Page 173; 460pp; English.

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             ABRS4277 represents a human trypsinogen protein given in comparison with
the human NOV35b protein in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis, Neisseria gonorrheae, antigen, vaccine, antigenic, diagnosis, immunogenic, infection, meningitis, septicaemia, antibacterial, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scarselli M;
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
sequences, which are used in examples from the present invention.
                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:916.
                                                                                     6; Length 531;
                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hickey E,
Ratti G,
                                                                                     Score 47; DB 6
Pred. No. 64;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 555; 1453pp; English.
                                                                                                                                                                                                                                                    AAY74721 standard; protein; 267 AA.
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, Pizza M, Rappuoli R,
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98US-0098994P.
98US-0099062P.
98US-0103749P.
                                                                                    56.0%;
66.7%;
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                                                                                                                                                                                                                                                                                                               21-MAR-2000 (first entry)
                                                                                                                    8; Conservative
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                                                                                                                                               4 MDPTPPLWIKTE 15
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Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                70 MDTSPPLWTLTE
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                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ53483.
                                                          Sequence 531 AA;
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Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999;
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                                            Conservative
                                                                              AKHPTPPTWLQT 20
                                                                3 AMDPTPPLWIKT 14
                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                    Query Match
Best Local Similarity
Matches 7; Conserv
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 Sequence 267 AA;
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                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions.
                                                                                                                                                                                                                               Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                ABB59797;
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AAR56496
ID AAR56
                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Neisserial polypeptides predicted to be useful antigens for
                                                                ÷
                                                                                                                                                                                                                              Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:910.
                                         DB 3; Length 267;
45;
                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galeotti C, Grandi G, Hickey E,
Pizza M, Rappuoli R, Ratti G,
Venter JC;
                                                                2; Mismatches
                                            Score 46;
Pred. No.
                                                                                                                                                              AAY74718 standard; protein; 267 AA.
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used in gene therapy protocols
                                                                                                                                                                                                                                                                                                                                                                                                98US-0094869P.
98US-0098994P.
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                                          54.8%;
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                                                                                                                                                                                                                                                                         antibacterial; gene therapy
                                                                                                                                                                                                          (first entry)
                                         Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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(GENO-) INST GENOMIC RES.
                                                                                                          AKHPTPPTWLQT 20
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                                                                                     3 AMDPTPPLWIKT 14
                                                                                                                                                                                                                                                                                               Neisseria meningitidis
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N-PSDB; AAZ53480.
                       Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                   WO9957280-A2.
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Petersen J,
Tettelin H,
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02-SEP-1998
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25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orosophila melanogaster polypeptide SEQ ID NO 6183
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Pred. No. 1.3e+02;
2; Mismatches 4;
DB 3;
Score 46; DB 3
Pred. No. 45;
2; Mismatches
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                                                                                                                                                                                                                                                                                        ABB59797 standard; protein; 729 AA.
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11-JUL-2000; 2000US-00614150.
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Screen for cpds, that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in disease.
               Drosophila TATA-binding protein associated factor dTAFII150 protein.
                                             Drosophila, TATA-binding protein, TBP associated factor, TFIID; RNA polymerase II, transcription, messenger RNA, nuclear fraction; holoenzyme, lambda-gt11; expression library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Col 123-132; 86pp; English
                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                          Dynlacht BD;
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-333245/33.
                                                                                                                                                                                                                                                                                                                           Hoey T,
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT42219
                                                                                                                                                                                                              28-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The TATA-binding protein associated factor hTAPISO (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific blochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology. (Updated on 25-MAR-2003 to correct PN
                                                                                                                            protein associated factor; dTAFISO; screening; diagnostic; gene transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, useful in screening, diagnostics and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanese N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.8%; Score 46; DB 2; Length 1189; Best Local Similarity 53.3%; Pred. No. 2.1e+02; Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comai L, Dynlact BD, Hoey T, Ruppert S, Weinzierl ROJ;
                                                                                            TATA-binding protein-associated factor dTAPISO.
                                                                                                                                                                                                                                                                /note= "Arg, Pro or His"
1172
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                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                          'note= "Val or Leu"
                                                                                                                                                                                                                                                                                                          note= "STOP"
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                                                               (first entry)
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                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1189 AA;
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                                                                                                                                                                                                          Key
Misc-difference
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                                                                                                                          TATA-binding
                                                                                                                                              therapeutic;
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                                           25-MAR-2003
23-MAR-1995
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                                                                                                                                                                            Drosophila
               AAR56496;
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Ruppert S, Weinzierl ROJ, Tjian R;

Tanese N,

94US-00188582.

93US-00013412 93US-00087119

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This is the amino acid sequence of the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFIIGO. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 60 kD by SDS-PAGE. The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II, the RNA transcription proceeds in vitro upon addition of several nuclear fractions designated TFIID, B, D, E, F, H, I and U to RNA polymerase II holoenzyme. Fraction TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID expression allowed cloning of the corresp. genes from lambda-gtil expression libraries. (Updated on 25-MAR-2003 to correct PF field.)
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nes 8; Conservative
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Gaps

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AAW06086 standard; protein; 1213 AA.

RESULT 15 AAW06086 (revised)
(first entry)

25-MAR-2003 27-JAN-1997

AAW06086;

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Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 1, Appli
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Sequence 278038,
Sequence 200494,
Sequence 16, Appl
Sequence 16, Appl
Sequence 255035,
Sequence 229035,
Sequence 25501, A
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(without alignments)
52.587 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/VEOT_REW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/REG_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/NEG_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NEGOT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/NEGOT_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/NEGOT_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-047-945-4
US-10-047-945-5
US-10-047-945-1
US-10-047-945-6
US-10-236-417-104
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US-10-424-599-278038
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US-10-424-599-229035
US-10-424-599-255201
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                  Scoring table:
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No.
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Sequence 114167,
Sequence 114167,
Sequence 197262,
Sequence 197265,
Sequence 73022, A
Sequence 731022, A
Sequence 75154, A
Sequence 75154, A
Sequence 1244200,
Sequence 126480,
Sequence 264272,
Sequence 264272,
Sequence 186583,
Sequence 186583,
Sequence 186583,
Sequence 186583,
Sequence 186583,
Sequence 186583,
                                                                                                                                                                                                                                                                   Sequence 1735, Ap
Sequence 161, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
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Sequence 824, App
Sequence 133075,
                              Sequence
Sequence
Sequence
                      Sequence
5 US-10-424-599-151167

5 US-10-424-599-205702

5 US-10-424-599-205702

6 US-10-424-599-283741

4 US-10-177-293-228

4 US-10-177-293-228

4 US-10-177-293-228

4 US-10-437-963-114467

6 US-10-437-963-114467

6 US-10-437-963-114467

6 US-10-282-122A-75189

6 US-10-282-122A-75189

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6 US-10-437-963-18480

6 US-10-437-963-18880

6 US-10-437-963-18880

7 US-10-767-701-54623

6 US-10-437-963-188412

6 US-10-437-963-188412

8 US-10-767-701-54623

6 US-10-437-963-188412

8 US-10-767-701-54623

8 US-10-767-701-54623

8 US-10-437-963-188412

8 US-10-764-875-824

9 US-10-276-774-1735

9 US-10-276-774-1735

9 US-10-20-808-112
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## ALIGNMENTS

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; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM ; OTHER INFORMATION: US 5,576,297. US-10-047-945-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Sequence 2, Application US/10047945

Sequence 2, Application US/2003015755A1

Sequence 2, Application No. US2003015755A1

SEREAL INPORMATION:

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: JAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1991 IMPLICATED DISORDERS)

FILE REFERENCE: FWLPAT015US

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: 2002-01-14

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 2

LENGTH: 15

TYPE: PRI

ORGANISM: Artificial Sequence
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100.0%; Score 84; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
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1 LKAMDPTPPLWIKTE 15

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Tue May 31 05:57:58 2005

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      Sequence 4, Application US/10047945
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; TITLE OF INVENTION: (IGE) IMPLICATED
; FILE REPERENCE: FWLPATOISUS
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR PILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR FILING DATE:
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100.0%; Pred. No. 0.0053;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 14;
Pred. No. 0.0015;
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100.0%; Pred. No. v.
0; Mismatches
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 5
LENGTH: 11
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US-10-047-945-1
; Sequence 1, Application US/10047945
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 12; Conservative
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Best Local Similarity
US-10-047-945-4
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US-10-047-945-5
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LOCATION:
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NAME/KEY:
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; General Information No. US2003015755A1
; General Information No. US2003015755A1
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: UDGONOSIS AND TREATMENT POR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (195) IMPLICATED DISORDERS
; FILE REFERENCE: FWLPATO15US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                               APPLICANT: LIPPS, FREDERICK W.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (1981) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATOISUS

CURRENT APPLICATION NUMBER: US/10/047,945

CURRENT PAPLICATION NUMBER: ...

PRIOR APPLICATION NUMBER: ...

PRIOR PLING DATE: 2002-01-14

PRIOR PLING DATE: ...

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 1

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence
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Pred. No. 1.3e+06;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
COTHER INFORMATION: SYNTHESIZED.
COTHER INFORMATION: US 5,576,297.
US-10-047-945-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Synthetic.
US-10-047-945-6
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US20030157555A1
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Best Local Similarity 100...
---- 9, Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Lou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Wi, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 200494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Acoustic David K
APPLICANT: Abou Vihua
APPLICANT: Cao Yongwei
TTILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TTILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.8%; Score 46; DB 16; Length 384; 58.3%; Pred. No. 1e+02;
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US-10-424-599-173148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_95958C.1.pep
US-10-437-963-200494
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                                                                                                               Sequence 200494, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 58.3.
Fig. 7, Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |||| : |
14 DPIPPLWAQPE
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US-09-885-303A-16
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROU YINUA
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION DATE: 130-21(53223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278038
LENGTH: 85
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                                       FILE REFERENCE: 21402-442C
CURRENT APPLICATION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442C
CURRENT PELING DATE: 2003-01-06
FRIOR PILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-07
FRIOR PILING DATE: 2001-09-07
FRIOR PILING DATE: 2001-09-07
FRIOR PILING DATE: 2002-03-05
FRIOR PILING DATE: 2002-03-05
FRIOR PILING DATE: 2002-03-05
FRIOR PILING DATE: 2002-03-07
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-17
FRIOR FILING DATE: 2001-09-17
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APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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Pred. No. 24;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_93091C.1.pep
US-10-424-599-278038
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 8, Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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MDTSPPLWTLTE 81
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TPPLWIKTE 15
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Sequence 229035, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRESENCE: 38-21 (5323) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

EBOG ID NO 229035
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
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                                                                                                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: MAP TO AL133458.11
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: SWISSPROT HIT: 053951, EVALUE 6.40e+00
OTHER INFORMATION: EST_HUMAN HIT: A19864481.1, EVALUE 6.00e-16
US-09-864-761-45321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%; Score 44; DB 15; Length 70; 60.0%; Pred. No. 40; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_48845C.1.pep
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 45321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 9
Pred. No. 22;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.4%;
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.4
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
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Sequence 45321, Application US/09864761
Sequence 45321, Application US/09864761
Sequence 45321, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                       GENERAL INFORMATION:
APPLICANT: TRAVIS,
TITLE OF INVENTION: METHADS AND COMPOSITIONS FOR THE TREATMENT OF MACULAR
TITLE OF INVENTION: AND RETINAL DEGENERATIONS
FILE REFERENCE: UTSD:758US
CURRENT PEPLICATION NUMBER: US/09/885,303A
CURRENT FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-01-23
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Pred. No. 1.2e+02;
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CURRENT APPLICATION NUMBER: US/09/664,761

CURRENT APPLICATION NUMBER: US/09/664,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELLING DATE: 2000-05-26

PRIOR PLLING DATE: 2000-05-26

PRIOR PLLING DATE: 2000-06-26

PRIOR PLLING DATE: 2000-06-26

PRIOR PLLING DATE: 2000-09-03

PRIOR PLLING DATE: 2000-09-03

PRIOR PLLING DATE: 2000-10-04

PRIOR PLLING DATE: 2000-10-04

PRIOR PLLING DATE: 2000-10-04

PRIOR PLLING DATE: 2001-01-04

PRIOR PLLING DATE: 2001-01-30

PRIOR PLLING DATE: 2001-01-30
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Best Local Similarity 57.1%;
Matches 8; Conservative
  Publication No. US20030032078A1
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268 LKAMDPSGSLYVRT 281
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bos taurus
US-09-885-303A-16
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US-10-424-599-205702
US-10-424-599-205702
Sequence 205702, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205702
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Can Vinua
APPLICANT: 
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Pred. No. 60;
1; Mismatches 0; Indels
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US-10-424-599-151167
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201
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CURRENT FILING DATE: 2003-04-28 WIMBER OF SEQ ID NOS: 285684 SEQ ID NO 255201 LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                 52.4%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DPTPPLWI 12
                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PTPPLWI 12
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92 PTPPLWV 98
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LOCATION: (1)..(144)
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                                                                                                                                                                                                                                           FEATURE:
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OTHER INFORMATION: Clone ID: PAT_MRT3847_27777C.1.pep

US-10-424-599-205702

Query Match

Guery Match

East Local Similarity 85.7%; Pred. No. 80;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

Oy 6 PTPPLWI 12

Db 28 PTPPLWV 34

Search completed: May 26, 2005, 19:17:13

GOMBER INFORMATION:

Search completed: May 26, 2005, 19:17:13
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Sequence 4103, Ap Sequence 104, App Sequence 14, Appl Sequence 2, Appli Sequence 7219, Ap Sequence 56512, A Sequence 21938, A Sequence 21938, A

42, Appî 14895, A

Sequence Sequence 6 Sequence 6 Sequence 1

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

Result

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Sequence 1, Application US/08310340A

Sequence 1, Application US/08310340A

Sequence 1, Application US/08310340A

Batent No. 5576297

GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS

TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSER: BINIE V. LIPPS

STREET: 4509 MINOSA DR.

COUNTRY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

COUNTRY: USA

STATE: TEXAS

COMPUTER: TEM COMPATIBLE

COMPUTER: 15 MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,340A

FILING DATE: 12 SEPTEMBER 1994

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 108/058, 387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: NAME: NAME: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: NAME
                                                        US-08-463-081B-14
US-08-461-379A-14
US-08-462-08-14
US-08-462-08-14
US-08-465-68-14
US-08-465-64-14
US-09-949-016-7619
US-09-949-016-7619
US-09-270-767-41296
US-09-252-991A-21938
US-09-252-991A-21938
US-09-252-991A-21938
US-09-252-991A-21938
US-09-328-352-6054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-857-224B-42
US-09-902-540-14895
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ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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TELECOMMUNICATION INFORMATION:
TELEBHONE: 713-723-6845
TELEBRAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: SINGLE TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
Sequence 1, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 1336, Ap
Sequence 1357, Ap
Sequence 43223, A
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1353, Ap
Sequence 44501, A
Sequence 44501, A
Sequence 44501, A
Sequence 44501, A
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15, Appl
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18, Appl
45215, A
1166, Ap
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                                                                                                                                                                                                                            May 26, 2005, 18:29:58; Search time 34.2 Seconds (without alignments) 32.741 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/pcTUS_COMB.pep:*
                                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-657-163A-1

US-08-646-715-20

US-09-646-715-20

US-09-134-000C-5938

US-09-134-000C-5938

US-09-732-210-1367

US-09-732-210-1367

US-09-732-210-1367

US-09-732-210-1353

US-09-737-767-43223

US-09-770-767-4255

US-09-270-767-4255

US-09-270-767-4255
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US-09-710-279-1166
US-09-248-796A-20923
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-09-710-279-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
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SEQUENCE CHARACTERISTICS:
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Sequence 1, Application US/08657163A
Sequence 1, Application US/08657163A
Sequence 1, Application US/08657163A
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: A509 MIMOSA DR.
CITY: BELLAIRE
STREET: TEXAS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 84; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              VOLUME: 10TH WORLD CONGRESS ON ANIMAL VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, VOLUME: SINGAPORE ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUE: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 18M COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOCTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FLING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/310,340
FILING DATE: 10 MAY 1993
APPLICATION NUMBER: 28,387
FILING DATE: 10 MAY 1993
APPLICATION NUMBER: 28,198
REGISTRATION NUMBER: PWL-PAT-US-011
TELEPHONE: 713-482-2961
                                          HAPLOTYPE:
TISSUE TYPE:
BLOOD
CELL LINE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
CLONE:
                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SENARE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
  TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LKAMDPTPPLWIKTE 15
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DATE: 3-1
US-08-310-340A-1
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Gaps
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CLONE:
PUBLICATION INFORMATION:
AUTHORS:
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08657163A
Patent No. 2544449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 84; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
                                                                                                                                                           OPOSSUM SERA: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
TYPE: ANALLY
STRANDENNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGNENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID
ORANISM: DIDELPHIS VIRGINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIPLCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIPLCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IE: BINIE V. LIPPS 4509 MIMOSA DR.
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                      HAPLOTYPE:
TISSUE TYPE: BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-8 NOV 1991
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STATE: TEXAS
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Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
                                                                                                                                                                                                                                                  620 LSAMDDSPVLWIRLD 634
       SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
                                                                                                                                                                                                              1 LKAMDPTPPLWIKTE 15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                              ; MOLECULE TYPE: protein US-08-188-582-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-646-715-20
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                                                             TOPOLOGY:
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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100.0%; Pred. No. 0.031;
tive 0; Mismatches 0; Indels
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4 Embarcadero Center, Suite 3400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A-57650-2/AJT/RAO
                                                                                                                                                                                                            SEQUENCE CALL TO LENGTH: 10
TYPE: AMINO ACID
STRANDENMESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
                                                                                                  FWL-PAT-US-011
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-482-2961
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NAME: Ogman, Richard A
REGISTRATION UNDRER: 36,627
REFERENCE/DOCKET UNDRER: A-576
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tjian, Robert
Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
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ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
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Best Local Similarity 100.
Matches 10; Conservative
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STATE: California
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-188-582-20
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Query Match

Gaet Local Sainlarity 53.34; Score 46; DB 1; Length 1213;

Matchee 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 620 LANDDSPUMIXED 634

RESULT 5

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RESULT 5

RESULT 5

RESULT 6

GREGATIS 60

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Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-09-732-210-1367
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LENGTH: 253
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US-09-036-987A-5
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                                                                                  Sequence 5938, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

Fatent No. 6617156

Fatent No. 6617156

Fatent No. 6617156

FATILE OF INVENTION: BUTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BUTENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BATE: 1998-08-13

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1997-08-15

FRIOR APPLICATION NUMBER: US 60/0S5,778

FRIOR PILING DATE: 1997-08-15

SOFTWARE PATENT NOS: 6812

SOFTWARE PATENT NOS: 6812

SEQ ID NO 5938

LENGTH. 137
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Sequence 13316, Application US/09902540

Sequence 13316, Application US/09902540

Batent No. 683347

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Misgand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: 08/09/902,540

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13316

LENGTH: 397
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Pred. No. 11;
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Pred. No. 68;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.6%;
75.0%;
  620 LSAMDDSPVLWIRLD 634
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Best Local Similarity 66.7%;
Matches 6; Conservative
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; ORGANISM: Myxococcus xanthus
US-09-902-540-13316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0°
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85 NPTPPLWV 92
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                                                           RESULT 6
US-09-134-000C-5938
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US-05-270-767-4323
US-05-270-767-4323. Application US/09270767
Sequence 43223. Application US/09270767
Sequence 43223. Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
SOFTWARE: PALENTIN VONS: 62217
SOFTWARE: PALENTIN Vor. 2.0
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APPLICANT: Baltz, Mary C.
APPLICANT: Exception, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald U.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: 39
CORRESPONDENCE ADDRESS: 39
CORRESPONDENCE ADDRESS: 30
ADDRESSER: Dow AgroSciences LLC Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
TITLE OF INVENTION: Acti-fungal Proteins and Methods for Their Use FILE REFERENCE: 38-21(15.056)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
LENGTH: 151
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STREET: 9330 Zionsville Road
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100.0%; Pred. No. ....
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Sequence 5, Application US/09603207B Patent No. 6521406
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Best Local Similarity
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21 TPPSWLKT 28
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV.
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
BARLIER APPLICATION NUMBER: US 09/36987
BARLIER APPLICATION NUMBER: US 09/36987
BARLIER PAPPLICATION OF: 39
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
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                                                                                            COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

CMBUTER IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COURREATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A

FILING DATE: 09-MAR-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
RAME: Stuart, Donald R:
REGISTRATION NUMBER: 28,479

REFERENCE/DOCKET NUMBER: 28,479

FELENCH NUMBER: 28,479

FELENCH NUMBER: 28,479

REFERENCE/DOCKET NUMBER: 28,479

FELENCH NUMBER: 28,479

FELENCH NUMBER: 28,479

REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09370700 Patent No. 6274350
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2850 LRAADVSAPLWLAT 2863
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2850 LRAADVSAPLWLAT 2863
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Matches 7; Conservative
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MOLECULE TYPE: protein
Indianapolis
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Matches 7; Conserva
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RESULT 12

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Factor No. 657361

GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.

APPLICANT: Mittanck, Cindy A.

APPLICANT: My Younie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use FILE REFREBRUCE: 38-21(15036)B

CURRENT PRICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 1353
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Kathryn C
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
ITILE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: SO489 DIV1
CURRENT APPLICATION NUMBER: US/09/603,207B
CURRENT FILING DATE: 2000-66-23
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
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48.8%; Score 41; DB 4; 1
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 3; Mismatches 4
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72;
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Pred. No.
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; Sequence 57545, Application US/09270767
: Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-603-207-5
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; ORGANISM: Agaricus bisporus
US-09-732-210-1353
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GENERAL INFORMATION
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RESULT 15
US-09-270-767-42501

Sequence 42501, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: HOMBURGER et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION UNDER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 42501

LENGTH: 303

LENGTH: 303

TYPE: PRT

CORRANISM: Drosophila melanogaster

US-09-270-767-42501
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PATENTI Ver. 2.0
; SEQ ID NO 57545
LENGTH: 198
; TYPE: RRT
ORGANISM: Drosophila melanogaster
; FRATURE:
; CATHER INFORMATION: Xaa means any amino acid
US-09-270-767-57545
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Pred. No. 95;
3; Mismatches 2; Indels
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Pred. No. 1.5e+02;
2; Mismatches 3; Indels
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Best Local Similarity 54.5%;
Matches 6; Conservative ;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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95 LQPTPELWTQT 105
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70 IKAVSPSPNLW 80
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 18:26:23 ; Search time 7.9 Seconds (without alignments) 60.897 Million cell updates/sec

US-10-047-945-3 24 Title: Perfect score:

1 LKAMD 5 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	86	٦,	AI1916	hypothetical prote
7	24	100.0	144	~	B83114	~
М	24	100.0	145	7	D83424	thetical p
4	24	100.0	178	N	A38593	=
υ	24	100.0	185	Н	LZWSG	lysozyme (EC 3.2.1
9	24	100.0	202	N	AE3377	queuine tRNA-ribos
7	24	100.0	210	~	T14734	NS5 protein - sorg
89	24	100.0	213	0	F69838	Lra
σ	24	100.0	237	N	A42013	alpha-1-B-glycopro
10	24	100.0	253	N	JC5709	maleate isomerase
11	24	100.0	256	N	C71546	probable glucose-6
12	24	100.0	270	Н	CCECID	cell division inhi
13		100.0	270	0	AH0724	um site d
14	24	100.0	270	N	F85695	division
15	24	100.0	270	~	E90837	
16	24	100.0	272	N	E95144	Cof family protein
17	24	100.0	272	N	C98012	conserved hypothet
18	. 24	100.0	279	N	S58402	synaptotagmin V -
19	24	100.0	304	~	I39049	alpha (1,3) fucosy
20	24	100.0	305	N	T09370	shikimate kinase h
21	24	100.0	306	N	B54717	Q.
22	24	100.0	359	~	A45156	(1,3)-
23	24	100.0	364	0	I39048	$\overline{}$
24	24	100.0	364	7	843117	transposase - Lept
25	24	100.0	374	N	H87450	conserved hypothet
56	24	100.0	377	N	AD3363	queuine tRNA-ribos
27	24	100.0	379	Н	DWDXBF	2-hydroxyglutaryl-
28	24	100.0	381	7	B69722	queuine tRNA-ribos
59	24	100.0	385	7	AD0528	conserved hypothet

hypothetical prote 3-ketoacyl-coa thi	hypothetical prote cellutagmin II syt arylsulfatase regu	phoH family protei transcription fact ATPase [imported]	ATPase - Chlamydop transcription fact transcription fact	cellobiose phospho phosphomannomutase	moaA/NirJ family F hypothetical prote
F90649 F75047	E/1113 F85500 S58400 D69525	F81552 S34449 C86504	B72118 A31752 S42111	C69785 G64349	D97243 T17332
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## ALIGNMENTS

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hypothetical protein as10884 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: A11916

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nak Res. 8 , 205-213, 2001 Nak Res. 8 , 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI1916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 «KUR>
A;Cross-references: UNIPROT:QGYYGG; GB:BA000019; PIDN:BAB72841.1; PID:g17130229; GSPDB:GA;Experimental source: strain PCC 7120

C, Genetics:

A;Gene: as10884 C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels

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1 LKAMD 5 ઠે

23 LKAMD 27 g

508 ribosomal protein L15 PA4244 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 1.5-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83114
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.X.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ..., Lorry, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho. A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: B83114
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kosidues: 1-144 CSTO>
A;Cross-references: UNIPROT:Q9HWF4; GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG0763
A;Experimental source: strain PAO1

A;Gene: rpl0; PA4244 C;Superfamily: Bscherichia coli ribosomal protein L15

05:58:04

Tue May 31

C; Accession: A00872; B34047

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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 LKAMD 46
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Cipacies: Peeudomonas aeruginosa
Cipacies: Peeudomonas aeruginosa
Cipacies: Desdep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cipace: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cipace: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Ristorer, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bi
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
I Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A.Reference number: A82950; MUID:20437337; PMID:10984043
A.Setatus: preliminary
A.Setatus: Drahamary
A.Setatus: Drahamary
A.Setatus: L-145 <STO>
A.Cross-references: UNIPROT:Q912X8; GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG0515
A.Gene: PA1761
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Cispecies: Masses; S19218
Rintchell, P.J.; Timmons, P.M.; Hebert, J.M.; Rigby, P.W.J.; Tjian, R.
Genes Dev. S. 105-119, 1991
A;Title: Transcription factor AP-2 is expressed in neural crest cell lineages during mou A;Reference number: A38593; MUID:91115091; PMID:198904
A;Accession: A38593
A;Accession: A38593
A;Accession: A38593
A;Accession: A38593
A;Coser-reference (1198/ment)
A;Residues: 1-178
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hypothetical protein PA1761 [imported] - Pseudomonas aeruginosa (strain PAO1)
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llarity 100.0%; Pred. No. 58;
Conservative 0; Mismatches 0;
Score 24; DB 2;
Pred. No. 47;
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Matches 5; Conservative 0;
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A;Molecule type: protein
A;Mesidues: 1-185 <61M-
A;Residues: 1-185 <61M-
A;Cross-references: UNIPROT:P00717
R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
B;Jahnen, W.; Ward, Commun. 166, 139-145, 1990
A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A;Reference number: A90157; MUID:90147691; PMID:2302197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes hydrolysis of the beta-1,4-glycosidic bond between N-acetylmura
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Kreywords: bacteriolytic enzyme; egg white; glycosidase; hydrolase; polysaccharide degr
F;4-60,18-29/Disulfide bonds: #status predicted
F;73,86/Active site: Glu, Asp #status predicted
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
J; Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessi
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens.
A;Reference number: AD3252; PMID:11756688
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A;Cross-references: UNIPROT:Q8YH02; GB:AE008917; PIDN:AAL52184.1; PID:g17982964; GSPDB:C
R;Simpson, R.J.; Begg, G.S.; Dorow, D.S.; Morgan, F.J.
Biochemistry 19, 1814-1819, 1980
Biochemistry 19, 1814-1819, 1980
A;Title: Complete amino acid sequence of the goose-type lysozyme from the egg white of A;Reference number: A00872; MUID:80198318; PMID:7378374
A;Accession: A00872
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14734
R;Sanan, N.; Azam, A.; Bhattacharya, A.; Sopory, S.K.
Submitted to the EMBL Data Library, December 1996
A;Reference number: Z18176
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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A;Residues: 'X',47-59,'X',61-68;95-99,'X',101-106,'X',108,'X',110-111 <JA2>
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100.0%; Pred. No. 66;
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RiHatakeyama, K.; Asai, Y.; Uchida, Y.; Kobayashi, M.; Terasawa, M.; Yukawa, H. Biochem. Biophys. Res. Commun. 239, 74-79, 1997
A;Title: Gene cloning and characterization of maleate cis-trans isomerase from Alcaligen A;Accession: UC5709; MUID:98005083; PMID:9345272
A;Accession: UC5709
A;Molecule type: DNA
A;Residues: 1-253 cHAT>
A;Residues: 1-253 cHAT>
A;Cross-references: UNIPROT:024766; DDBJ:AB005051; NID:g2575786; PIDN:BAA23002.1; PID:g2
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R;Stephens, R.S; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809; PMID:9784136
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A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Alcaligenes faecalis
C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 09-Jul-2004
C;Accession: JC5709; PC4412
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-25 <HA2>
C;Comment: This enzyme catalyzes the conversion of maleate to fumarate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 256;
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cell division inhibitor minD - Escherichia coli (strain K-12)
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                                                                                                                                                                                                                                                                                                                                                                                           - Alcaligenes faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: Alcaligenes faecalis maleate isomerase C;Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 24; DB
100.0%; Pred. No. 83;
tive 0; Mismatches
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       red. No. 78;
Mismatches
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100.0%; Pred. No. 8
           100.08;
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C;Superfamily: yeast SOL3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maleate isomerase (EC 5.2.1.1)
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                                               5; Conservative
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       Best Local
Matches
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C;Species: Sacillus subtilis
C;Species: Sacillus subtilis
C;Species: Sacillus subtilis
C;Species: Sacillus subtilis
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, S.; Brusich, S.D.; Brunerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Burlors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, S.; Authors: Lauber, J.; Lazarevic, V.; Ete, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell, Koetter, P.; Koningsein, G; Kooda, E.; Roche, B.; Roche, M.; Sadaie, Y.; Bohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Roche, M.; Sadaie, Y.; Sanlon, A;Authors: Schleich, S.; Schroeter, R.; Soche, B.; Roche, M.; Sadaie, Y.; Sanlon, A;Authors: Schleich, S.; Schroeter, R.; Soche, B.; Tognoni, A.; Tosato, T.; Schroeter, R.; Yoshikawa, H.; Danchin, A.; Tamakoshi, A.; Amamoto, H.; Yamanoto, H.; Yamanoto, H.; Yamanoto, H.; Yamanoto, H.; Apareterium Bacillus subtilis. A;Reference number: Assettine sequence of the Gram-positive bacterium Bacillus subtilis. A;Recensesion: F69838
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Redius: Prelius preliminary; Pub.
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A;Experimental source: strain 168
C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1.210 <SAN>
A;Residues: 1.210 <SAN>
A;Coss-references: UNIPROT:P93525; EMBL:Y09874; NID:e1012757
A;Experimental source: variety Tx430; leaf
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Matches 5; Conservative
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C; Superfamily: cell division inhibitor minD
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Best Local Similarity 100..
Best Local S; Conservative
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Best Local Similarity
5; Conserv?
LKAMD 113
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A;Molecule type: DNA
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                                                                  Cipate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
Cipate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
Cipate: 30-Jun-1990 #sequence_revision 18463
Ride Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
Cell 56, 641-649, 1989
A.Title: A division inhibitor and a topological specificity factor coded for by the mini
A.Reference number: A31877; MUD:89136010; PMID:2645057
A.Reference number: A31877; MUD:89136010; PMID:2645057
A.Residues: 1-270 < DEB>
A.Residues: 1-270 < DEB>
A.Residues: 1-270 < DEB>
A.Fesidues: 1-270 < DEB>
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-270 <BLAT>
A;Cross-references: GB:AE000216; GB:U00096; NID:g1787417; PIDN:AAC74259.1; PID:g1787423;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Description: a membrane ATPase required for correct placement of cell division site A; Note: minC and minD act in concert to form an inhibitor capable of blocking formation for found between ffsz and minCD C; Superfamily: cell division inhibitor minD C; Keywords: ATP; cell division control; nucleotide binding; P-loop F;10-17/Region: nucleotide-binding motif A (P-loop) F;16/Binding site: ATP (Lys) #status predicted
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-270 <PA>
A;Coss-references: GB:AL513382; PIDN:CAD05498.1; PID:g16503002; GSPDB:GN00176
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 24; DB 2; Length 270; Best Local Similarity 100.0%; Pred. No. 89; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 270;
89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fitle: The complete genome sequence of Escherichia coli K-12; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
Alternate names: septum site-determining protein minD
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100.0%; Pred. No. 89;
ive 0; Mismatches
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C; Superfamily: cell division inhibitor minD
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Riperra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 201
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-270 <STO>
A,Cross-references: UNIPROT:P18197; GB:AE005174; NID:g12514869; PIDN:AAG56026.1; GSPDB:G
A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Species: Escherichia coli
C. Species: Escherichia coli
C. Species: Bscherichia coli
C. Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C. Accession: E90837
R. Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A. Arithe: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A. Accession: E90837
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A;Cross-references: UNIPROT:P18197; GB:BA000007; PIDN:BAB35092.1; PID:g13361133; GSPDB:CA;Experimental source: strain 0157:H7, substrain RIMD 0509952
division inhibitor minD - Escherichia coli (strain O157:H7, substrain EDL933)
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                                  C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85695
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Pred. No. 89;
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100.0%; Pred. No. 89;
iive 0; Mismatches
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May 26, 2005, 18:18:07; Search time 38.2 Seconds (without alignments) 67.026 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                        Run on:
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US-10-047-945-3 24 Title: Perfect score: Sequence:

1 LKAMD 5 Scoring table:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1612378 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Q9tr78 didelphis m	Q27566 dictyosteli	Q72nv8 leptospira		_				Q8yyg6 anabaena sp	Q93ce7 anabaena va	Q8gu99 oryza sativ		Q8xjc6 clostridium		-	Q8hz75 didelphis m	Q37950 lactococcus	Q889v2 pseudomonas	Q88q16 pseudomonas	_	Q9i2x8 pseudomonas	Q655r8 oryza sativ	eulemur	Q8wmu9 eulemur ful	Q8wnn7 varecia var	Q8wnn8 varecia var	P00717 cygnus atra	Q8yh02 brucella me	006732 bacillus su		Q8nie7 glomus intr
SOFTWARES	ID	Q9TR78	Q27566	Q72NV8	Q72TL6	Q6MJ74	Q82K17	Q8F7M0	Q80VT8	QBYYG6	Q93CE7	Q8GU99	Q54772	Q8XJC6	Q72LB6	Q8EQE9	Q8HZ75	037950	Q889V2	двволе	Q9HWF4	Q912X8	Q655R8	QSWMUS	Q8WMU9	Q8WNN7	Q8WNN8	LYG CYGAT	Q8YH02	006732	Q9AGS2	Q8NIE7
	DB	2	N	7	7	7	~	~	7	N	~	0	7	~	7	~	N	~	N	~	7	N	7	0	~	7	~	н	~	~	N	7
	Query Match Length	17	25	59	62	99	69	69	92	98	66	107	120	120	125	133	140	142	144	144	144	145	166	180	180	180	180	185	202	213	226	227
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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	Result No.	7	73	m	4	ហ	ø	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31

Q8nj35 glomus intr Q8nj36 glomus intr	~a 13	P93525 sorghum bic Q84wd9 arabidopsis	_	Q91155 rhodobacter O24766 alcaligenes	Q9z5q1 clostridium Q9pkk7 chlamydia m	٠	Q9vwa8 drosophila
Q8NJ35 Q8NJ36	Q8NJ37 Q65N09	P93525 Q84WD9	Q62WW5	09F155 024766	Q9Z5Q1 6PGL CHLMU	6PGL_CHLTR 0651.H4	FRG1_DROME
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227	227	235	247	251	254 256	256	262
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
24	24 24	2 2 4 4	24	2 2 4 4	2 2 4 4	2 2 4 4	24
32	3.4 3.5	36	38	40	41 42	43	45

# ALIGNMENTS

SUL FR7		ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).	Didelphis marsupialis (Southern opossum). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	eria; Didelphimorphia; Didelphidae;	NCB1_1dX1D=9268; [1]	SEQUENCE.	mbDLINE=93149299; ruomeu=7846694; DOL=10.1016/0041-0101(94)90353-0; Perales J., Moussatche H., Marandoni S., Oliveira B., Domont G.B.:	"Isolation and partial characterization of an anti-bothropic complex	from the serum of South American Didelphidae.";	TOXICON 32:123 -1249(1594). SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;	Query Match 100.0%; Score 24; DB 2; Length 17; Best Local Similarity 100.0%; Pred. No. 29; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps	1 LKAMD 5	1 LKAMD 5	лт 2	. add . variation 22300	i verminani i	(TrEMBLrel.	(TrEMBLrel. 01,	(TrEMBLrel. 26, Last annotation	pyrophosphorylase (EC 2.7.7.9)	namme-optofic) Dictrostelium discoideum (Slime mold)	Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.	N/DI Tavid-44600.	RESULT OOD TOO TOO TOO TOO TOO TOO TOO TOO TOO	1.7 1  78  79  79  79  79  79  79  79  79  70  70	PRELIMINARY;  (TrEMBLrel. 13,  (TrEMBLrel. 16,  TremBlrel. 16,  TremBlrel. 16,  TremBlrel. 16,  TremBlrel. 16,  TremBlrel. 16,  TremBlrel. 16,  12569;  PubMed=784  Moussatche H., M  Moussatche H., M  Moussatche H., M  Moussatche H., M  The Americal Chara  The Americal Conservative  The American Conservative  The	Created) Last seque Last annol ON SUBUINT hern opossis a; Craniats phimorphia Ade94; DOI: Marangoni ( acterizati rican Dide: CB55FB40i ; Score 2, ; Pred. N O; Mismai PRT; Created) Last seque Last annol Se (EC 2.7;	17 AA.  lence update)  teation update)  r (Fragment).  au. (Stragment).  i. Didelphidae; Didelphis.  s. Oliveira B., Domont G.B.;  con of an anti-bothropic complex.  lence of an anti-bothropic complex.  lence an anti-bothropic complex.  lence an anti-bothropic complex.  lence of an anti-bothropic complex.  lence an anti-bothropic complex.  lence an anti-bothropic complex.  lence of an anti-bothropic complex.  lence update)  lence update)
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SEQUENCE FROM N.A.

Moon B.-C., Haribabu B., Dottin R.P.;

Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; L28007; AAA91057.1; -.

DictyBase; DDB0214911; ugpB.

DictyBase; DDB0214911; ugpB.

GO; GO:0016740; Fttranferase activity; IEA.

GO; GO:0003983; F:UTP-gJucose-1-phosphate uridylyltransferase. . .; IEA.

GO; GO:0003152; P:metabolism; IEA.

InterPro. J PR002518; UDPGP, trans.

Pfam; PF01704; UDPGP, 1.

Pfam; PF01704; UDPGP, 1. 

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PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
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01-JUN-2003
01-JUN-2003
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Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

Nascimento A.L.T.O., Yo. A.I., Martins E.A.L., Monteiro-Vitorello C.B.,

Narques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,

Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,

Perro E.S., Ferro M.T., Furlan L.R., Gamberini M., Giglioti E.A.,

Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.T.,

Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,

de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,

A. Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,

Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;

T. "Comparative genomics of two Leptospira interrogans serovars reveals

"T. "Comparative genomics of two Leptospira interrogans serovars reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                               Copenhageni).
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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                                                  Length 52;
                                                                           0; Indels
 1 1
52 52
52 AA; 5818 MW; CCC3C65E75DBA935 CRC64;
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                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insights into physiology and pathogenesis."; cteriol. 186:2164-2172(2004).
                                                100.0%; Score 24; DB 2;
100.0%; Pred. No. 95;
tive 0; Mismatches 0
                                                                                                                                                                                         59 AA
                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                        Transposase, IS1533.
OrderedLocusNames=LIC12721;
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Best Local Similarity 100.
Matches 5; Conservative
                                                 Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                         STRAIN-Fiocruz L1-130;
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05-JUL-2004
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Nascimento A.L.T.O., Ko.A.I., Martins B.A.L., Monteiro-Vitorello C.B., Marques M.V., Oliveira M.C., Menck C.P.M., Leite L.C.C., Carrer H., Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A., Goses-Neto A., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura B.T., Kuramae E.E., Lemos B.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Camargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A., Camargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A., Camargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A., Comparative genomics of two Leptospira interrogans serovars reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from predator unmasked: life cycle of Bdellovibrio bacteriovorus from Science 303:689-692(2004).

EMBL: BXB42554; CAE80687.1; -. CCmplete proteome.

SEQUENCE 66 AA; 8142 MW; 04D5D62C458E6ACD CRC64;
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STRAIN=HDL00 / DSM 50701 / ATCC 15336 / NCIB 9529;
STRAIN=HDL00 / DSM 50701 / ATCC 15336 / NCIB 9529;
Pubmed=14752164; DOI=10.1126/science.1093027;
Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
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Pfam; PF02311; Transposase_20; 1.
Complete proteome.
SEQUENCE 62 AA; 7499 MW; C79940DB51F0CAC2 CRC64;
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Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=Bd2909;
                                                                                                                                                                                                                                                                                                                                                                                                         novel insights into physiology and pathogenesis.";
J. Bacteriol. 186:2164-2172(2004).
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(TrEMBLrel. 24,
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Matches 5; Conservative
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Best Local Similarity
Matches 5: Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watenabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 2; Length 98; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 24; DB 2; Length 92; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley; TISSUE-Ventral prostate;
Oram S.W., Haleem R., Cai X., Cyriac J., Wang Z.;
Submitted (EGC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY195741; AAO40742.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Iron, Iron-sulfur; Metal-binding. SEQUENCE 98 AA; 10555 MW; 6D2CB4906B892AEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 AA; 10910 MW; 0C406A170449BC19 CRC64;
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GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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DNA Res. 8:205-213(2001).
Bubi, AP003583; BAB72841.1; -.
PIR; AI1916; AI1916.
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OrderedLocusNames=asl0884;
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Best Local Similarity luv...
5, Conservative
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les 5; Conservative
                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                       67
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Wh. H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-P.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
                                                                                                                                                                                                          Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.2.11433198;
Omura S., Ikeda H., Ishikawa J., Hanancto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
             OrderedLocusNames=SAV2586;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                               Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
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EMBL; AE011276; AAN48123.1; -.
Complete proteome.
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Hypothetical protein.
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hes 5; Conserv
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STRAIN=56601 / Ser
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Q8F7M0; Q8F7M0

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Local Similarity
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SEQUENCE FROM N.A.
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                                                                                             NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flesh-eater."
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05-JUL-2004
                                                                                                                                                                                                                                                                                           Query Match
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                             Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=1172;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu S., Xu Z., Xue H.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ495798; CAD44621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AA; 11685 MW; 4899ACD54BE73D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IRR001041; Ferredoxin. InterPro; IRR010111; Ferri 1. Iron; Iron-sulfur; Metal-binding. SEQUENCE 99 AA; 10702 MW; E3E3CCBA7E8B892A CRC64;
                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MYB29 protein (Fragment).
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
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Pred. No. 1.9e+02;
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100.0%; Pred. No. 1.-
0; Mismatches
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                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                            EMBL; AF410434; AAL05047.1;
HSSP; P80306; 1E9M.
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Best Local Similarity 100..
                                                                         PRELIMINARY;
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                                                                                                                                                                                         Anabaena variabilis.
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 29413;
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SEQUENCE
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093CE7
AC 093CE7
DT 01-DE 01-DE DT 01-
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Q8GU99
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Q54772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                              Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria, Cyanobacteria, Chrococcales, Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 2; Length 120;
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 120;
                                                                                                                                                                                                                               STRAIN=PCC 7942;
Phung L.T., Haselkorn R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59237; AAB82030.1; -.
Hypothetical protein.
SEQUENCE 120 AA; 13515 MW; 91DDAF420ECFB6B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Hypothetical protein.
SEQUENCE 120 AA; 13909 MW; 063865C7F7FB1632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical cytosolic protein.
OrderedLocusNames=TTC0143;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
11-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CPE1834.
OrderedLocusNames=CPE1834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 24; DB 2; I
100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0;
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EMBL; AP003192; BAB81540.1; -.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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                               01-OCT-2003 (TrEMBLre Hypothetical protein.
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MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
environments.";
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                                                                                      Henne A., Brueggemann H., Raaach C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
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01-MAR-2003 (TrEMBirel. 23, Last sequence update)
01-MAR-2004 (TrEMBirel. 26, Last annotation update)
01-MAR-2004 (TremBirel. 26, Last annotation update)
Cytidine:deoxycytidine deaminase (EC 3.5.4.-).
Name=cdd; OrdaredLocusNames=OB1751;
Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 24; DB 2; Length 125; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AA; 13658 MW; 77B2D52BCA699896 CRC64;
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BMBL; AP004598; BAC13707.1; -. HSSP; P19079; JUTK.

GO; GO:00126; F:cytidine deaminase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0068270; F:sinc ion binding; IEA.

GO; GO:006870; F:cytidine metabolism; IEA.

InterPro; IPR006262; Cyt deam tetra.

InterPro; IPR001215; GVPF (cyt deam.

PERO; GO:009031; GVPF (cyt deam.

PERO; ICRO1384; CVPT deam.

PROSITE; PS009031; CYT_DCMP_DEAMINASES; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 133 AA.
                                                                                                                                                                                                                                                      thermophilus.";
Nat. Biotechnol. 22:547-553(2004).
Bmbi, AEO17301; AAS80491.1;
InterPro; IPR002744; DUF59.
Pfam; PF01883; DUF59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD005595; DUF59; 1.
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Best Local Similarity 100،۰۰
است ما 5، Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                 SECUENCE FROM N.A.
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SEQUENCE 125 AA
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SEQUENCE 133 AA
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                                                               PubMed=15064768;
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Search completed: May 26, 2005, 18:43:23 Job time: 41.2 secs

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version	- 2005
GenCore	(c) 1993
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protein search, using sw model OM protein -

Run on:

26, 2005, 18:17:22 ; Search time 43 Seconds (without alignments) 44.972 Million cell updates/sec

US-10-047-945-3 24

1 LKAMD 5 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg seg . B B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aaw53842 N-terminu	Abb80224 Synthetic	Abb80228 Synthetic	Abb80227 Synthetic	Aaw53843 N-terminu		Abb80226 Synthetic	Abb80225 Synthetic	Aaw11575 N-termina	Aaw53841 N-terminu	Abb80223 Synthetic	Aab53797 Human col	Aab52152 Human sec	Aab52151 Human sec	Abg12903 Novel hum	Add29464 Mouse cae	Abp64620 Human ORF		Aau33664 Pseudomon	Abu39905 Protein e	Abu42143 Protein e	Abu15537 Protein e	Abo72633 Pseudomon	Aau19728 Human nov	Aau87551 Novel cen
ΙD	AAW53842	ABB80224	ABB80228	ABB80227	AAW53843	ABB80222	ABB80226	ABB80225	AAW11575	AAW53841	ABB80223	AAB53797	AAB52152	AAB52151	ABG12903	ADD29464	ABP64620	AAB20323	AAU33664	ABU39905	ABU42143	ABU15537	AB072633	AAU19728	AAU87551
DB	7	7	7	7	7	7	7	7	~	7	7	m	m	ო	4	7	ហ	4	4	9	9	9	7	4	4
Length DB	2	5	œ	9	10	10	11	12	15	15	15	42	70	70	105	105	112	141	144	144	144	144	145	148	148
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
Result No.	-	7	3	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abp47948 Human pol Adc10910 Human ext Add54866 Novel hum Add54566 Novel hum Abb81340 Pseudomon Aau87253 Novel cen Add54568 Novel hum Adn17855 Bacterial Aau11847 Human nov Aau8753 Novel cen Abp48067 Human pol Adc11029 Human pol Adc11029 Human pol Adc11029 Human the Adm87718 Human the Adm87718 Human the Adm87718 Human the Adm87718 Human Nov Add139310 S. Human Nov Add139310 S. Human Nov Add139310 S. Human Nov	Adn24398 Bacterial
ABP47948 ADC10910 ADC10910 ADC18866 AAU87251 AD154568 AAU87253 AAU87253 AAU19847 AAU87553 AAP48067 AAU87553 AAP48067 AAU1029 AD11029 AD11029 AD11029 AD11029 AD13910 ADN39110 ADN39110	ADN24398
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11444 11198668888 20009999999999999999999999999999999	234
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## ALIGNMENTS

LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment. AAW53842 standard; peptide; 5 AA. N-terminus of opossum LTNF. (first entry) 08-JUL-1998 AAW53842; AAW53842 

Didelphis virginiana.

US5744449-A.

28-APR-1998.

96US-00657163, 03-JUN-1996; 93US-00058387, 94US-00310340, 10-MAY-1993; 22-SEP-1994;

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps FW, Lipps BV;

WPI; 1998-271108/24.

Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.

Claim 5; Col 13; 11pp; English.

This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Rlapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

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Gaps

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Score 24; DB 7; I Pred. No. 1.8e+06; ; Mismatches 0;

0;

Conservative

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LKAMD LKAMD

Similarity 5; Conserva

100.0%; 100.0%;

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(first entry)

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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemeic lugus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                             ABB80228 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2003; 2003WO-US001044.
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic LTNF, LT-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003060471-A2.
                        Sequence 5 AA;
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                                                          Query Match
                                                                                   Local
                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                             ABB80228
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can be synthetically prepared rather than the horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                     Length 5;
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                                                                                                                   Score 24; DB 2; I
Pred. No. 1.8e+06;
                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      ABB80224 standard; peptide; 5 AA.
                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
snake. Being short it current production in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic LTNF, LT-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipps BV, Lipps FW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                          to horse proteins
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                                                                                                                                                                                                                                       LKAMD 5
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                                                                               Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              saliva; ELISA
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                           Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 4; 24pp; English.
                                                                                                                                                           Lipps BV, Lipps FW;
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(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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Gaps

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor factor (ITMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin & (IgE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or dedpression: The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifiged immediately, whereas blood requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogram's syndrome; Reiter's syndrome; Grayes' disease; Addison's disease; Hodgkin's disease; depression;
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                                           Length 8;
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                                                                                                          0; Indels
                                100.0%; Score 24; DB 7; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80227 standard; peptide; 9 AA.
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Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                 LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the peptide of the invention. It is a Lethal Toxin Neutraliaing Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Blapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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                                                                                                        AAW53843 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                            96US-00657163
                                                                                                                                                                                                                                                                                  histamine reaction treatment
                                                                                                                                                                                                     N-terminus of opossum LTNF.
                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                 Didelphis virginiana.
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LKAMD
                             LKAMD
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22-SEP-1994;
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                                                                                                                                         AAW53843;
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ID ABB8
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Gaps

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid archritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;

Synthetic LTNF, LT-11.

14-JAN-2003; 2003WO-US001044. 14-JAN-2002; 2002US-00047945.

WO2003060471-A2.

24-JUL-2003

saliva; ELISA

Graves'

Synthetic.

Lipps BV, Lipps FW; WPI; 2003-636703/60.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (ISE), nerve growth factor (NGF), insulin, myoglobin and/or adenosinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum ISE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be contrifiged immediately, whereas blood requires
                                                                                                                al toxin neutralising factor; LTNF; serum protein; immunoglobulin E; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; asthma; diabetes; autoimmune disease; systemic lugus erythematosus; rheumatoid arthritis; Sjogran's syndrome; Reiter's syndrome; se' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clotting time before centrifugation to separate serum. Saliva proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 7; Length 10; 100.0%; Pred. No. 25; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 3; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-2002; 2002US-00047945
                                     (first entry)
                                                                                                              toxin neutralising
                                                                                                                                           :gE; nerve growth factor;
                                                                            Synthetic LINF, LT-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipps BV, Lipps FW;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                      saliva; ELISA.
                                     06-NOV-2003
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ABB80222;
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                                                                                                                    Lethal
                                                                                                                                                                              SLE;
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Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a

Claim 7; Page 4; 24pp; English.

patient.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (1gE), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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Gaps

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5; Conservative

1 LKAMD 5

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ABB80226 standard; peptide; 11 AA.

(first entry)

06-NOV-2003

ABB80226;

Didelphis virginiana.

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoplobulin E (1gE), merve growth factor (MCF), insulin, myoglobin and/or adenosinase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. aethma, arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, at Addison's disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifugation to separate serum Saliva proteins
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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 4; 24pp; English
                                                                                                                                                                                                                                          14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                14-JAN-2002; 2002US-00047945.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                           Lipps BV, Lipps FW;
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Best Local Similarity
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                                                                                            saliva; ELISA
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20-MAR-1997
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                                                                                                                                Synthetic.
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNP). The use of purified LTNP or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNP and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ant of victims of bee or scorpion stings or plant or bacterial - by admin. of lethal toxin-neutralising factor or its N-terminal
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100.0%; Pred. No. 37;
tive 0; Mismatches
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                                                                                                                                                                                                  94US-00310340.
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94US-00310340.
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Best Local Similarity
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LIPPS F W.
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22-SEP-1994;
                                                                                  US5576297-A.
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Claim 11; Page 1918; 2104pp; English.
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                                                                                                                                                                                                                                            This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                  Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Query Match
Best Local Similarity 100.vv
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                                            Lipps BV;
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                                                                                         WPI; 1998-271108/24
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(LIPP/) LIPPS F W.
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                                          Lipps FW,
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (INTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E [1gE], nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, colon cancer, colon cancer antigen, diagnosis, detection, identification, cytostatic, cardioactive, neuroprotective, vulnerary, immunomodulatory, muscular, gynaecological, gastrointestinal, nephrotropic, antilnfective, antibacterial, gene therapy, wound; neural disorder, immune system disorder, muscular disorder, reproductive disorder, gastrointestinal disorder, renal disorder;
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Claim 3; Page 3; 24pp; English.
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nes 5; Conserv
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and (ant)agonists are useful in the diagnosis, treatment and prevention

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The poteins and autibodies to the proteins are useful for the prevention, colon disorders, and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, reproductive disorders, gastrointestinal cardiovascular disorders. AAC9874 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; anticorvulsant; antibecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 3; Length 42; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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Query Match
Best Local Similarity 100.00
Best Local Similarity
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The invention relates to the isolation of genes AAC96900-C96947 encoding the human secreted proteins AAB52104-B52150. This sequence was used as a query sequence for BLASTX searches. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies

preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.

WPI; 2000-656324/63

Disclosure; Page 447; 478pp; English.

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                               of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epileps; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70 AA;
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal gene; (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food sequence in tissue, as molecular weight markers and as food in suppliement. (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in polypeptide and polynuclectide sequences have applications in capposition of markers and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences of Acts and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping; gene mapping; gene therapy, forensic,
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                 Length 70;
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                       ABG12903 standard; protein; 105 AA.
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23-AUG-2000; 2000US-00649167.
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N-PSDB; AAS77090.
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                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                         Sequence 70 AA;
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Query Match 100.0%; Score 24; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 LKAMD 5
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29 LKAMD 33

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/NSO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/NSO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/NSO8_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0P_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOOP_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1462099 seqs, 344972447 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3, Appli	Sequence 7, Appli		Sequence 1, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1337, Ap	Sequence 1337, Ap	Sequence 10123, A	Sequence 187934,	Sequence 148579,	Sequence 41212, A
	QI	US-10-047-945-3	US-10-047-945-7	US-10-047-945-6	US-10-047-945-1	US-10-047-945-5	US-10-047-945-4	US-10-047-945-2	US-09-925-299-1337	US-09-925-299-1337	US-10-156-761-10123	US-10-424-599-187934	US-10-424-599-148579	US-10-767-701-41212
	g	14	14	14	14	14	14	14	0	10	14	15	15	16
	Query Match Length DB	ß	80	Q	10	11	12	15	42	42	69	70	98	98
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	24	24	24	24	24	24	24	24	24	24	24	24	24
	Result No.	1	7	٣	4	S	9	7	œ	6	10	11	12	13

Sequence 34493, A	Sequence 40, Appl	Sequence 1980, Ap	Sequence 275786,	Seguence 183694,	Seguence 5160, Ap	Seguence 43461, A		Seguence 70067, A	Sequence 378, App	Sequence 1069, Ap	Sequence 378, App	9567,	Sequence 769, App	771,	Sequence 508, App	497, 2	Sequence 1071, Ap	Sequence 497, App	-	28,	Sequence 70803, A	Sequence 152, App	Sequence 4295, Ap			665,	Sequence 154522,	Sequence 43262, A	Sequence 4, Appli	Sequence 71, Appl	Sequence 74006, A
16 US-10-767-701-34493	15 US-10-449-857A-40	₽	L5 US-10-424-599-275786	15 US-10-424-599-183694	) US-09-815-242-5160		15 US-10-282-122A-67829	US-1	9 US-09-764-870-378	L1 US-09-764-875-1069	L4 US-10-125-540-378	L7 US-10-732-923-9567	11 US-09-764-875-769	L1 US-09-764-875-771	LS US-10-369-493-508	9 US-09-764-870-497	L1 US-09-764-875-1071	14 US-10-125-540-497		LS US-10-210-172-58	L5 US-10-425-114-70803	US-1	LS US-10-369-493-4295	_		11 US-09-764-875-665	LS US-10-424-599-154522	16 US-10-767-701-43262	L3 US-10-067-989-4	us-	15 US-10-282-122A-74006
103	105	112	126	127	144	144	144	144	.148	148	148	151	166	199	205	208	208	208	213	225	230	231	234	234	234	239	244	244	270	272	272
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM ; OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Sequence 3, Application US/10047945
; Publication No. US2030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFRENCE: FWILPATOISUS
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 5
; LENGTH: 5
; LENGTH: 5
; TUPE: DOWN
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100.0%; Score 24; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
OOGANIDM: Artificial Sequence
FEATURE:
NAME/KEY:
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US20030157555A1

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                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above. US-10-047-945-7
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       Sequence 7, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E FILE REFERENCE: FWLPATION: (1gE) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATION UNMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10047945

Publication No. US2003015755A1

GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS

TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
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100.0%; Pred. No. 1.3e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 14;
Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Scortino. 100.0%; Pred. No. 100.0%; Mismatches
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CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
LENGTH: 9
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
EBNOTH: 8
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US-10-047-945-1
; Sequence 1, Application US/10047945
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; OTHER INFORMATION: Synthetic.
US-10-047-945-6
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-047-945-6
US-10-047-945-7
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APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (LGB) IMPLICATED DISORDERS
FILE REPERENCE: FWLPATOISUS
CURRENT PPLIACATION NUMBER: US/10/047,945
CURRENT FILING DATE: 202-01-14
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 5.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DISGOULIN E
FILE REFERENCE: FWLPATOISUS
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE:
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10047945
Publication No. US20030157555A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5, Conservative
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Matches 5; Conserv
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US-10-047-945-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1337
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Sequence 1337, Application US/09925299

Publication No. US20030040617A9

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO2

FILE REPERENCE: PAIO2

CURRENT APPLICATION NUMBER: US/09/925, 299

CURRENT PILING DATE: 2001-08-10

FRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0

FROUTH OF 1337
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100.0%; Pred. No. 82;
tive 0; Mismatches
                                                                                          CURRENT APPLICATION NUMBER: US/09/925,299;
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05883;
FRIOR PILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 1556;
SOFTWARE: Patentin Ver: 2.0
LENGTH: 42
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Best Local Similarity 100.
نم 5، Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4
APPLICANT: LIPPS, BINIE V.

APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIGGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: (198) IMPLICATED DISORDERS

FILE REFERENCE: FWLPATO15US

CURRENT APPLICATION NUMBER: U$/10/047,945

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 4

LENGTH: 12

TYDE: ...
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APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
CURRENT PRINGATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR PLILING DATE: 2002-01-14
PRIOR PLILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 14; Length 12; 100.0%; Pred. No. 22; 0; Indels tive 0; Mismatches 0; Indels
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Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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NAME/KEY:
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TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
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Best Local Similarity
Matches 5; Conserv
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Sequence 187934, Application US/10424599
Sequence 187934, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids MAME/KEY: SITE LOCATION: (34) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids acids
                                                                                                                                                                                                                                       DOCATION: (40); (40); JOHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1337
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                      LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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Similarity 100.0%; Pred. No. 1.4e+02;
5; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 10 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10123
LENGTH: 69
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APPLICANT: HORITAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-156-761-10123
Sequence 10123, Application US/10156761
Publication No. US20030119018A1
GENERAL INCERNATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                        LOCATION:
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Ynhua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 148579
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APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CURRENT APPLICATION DUMBER: US/10/767,701
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US-10-424-599-187934
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US-10-424-599-148579
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(70)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
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FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187934
LENGTH: 70
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 100...
5, Conservative
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Sequence 34493. Application US/10767701
Publication No. US20040172684A1
Fublication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53555)
CURRENT APPLICATION NUMBER: US/10/70,701
CURRENT APPLICATION NUMBER: US/10/70,701
SEQ ID NOS: 63128
SEQ ID NOS: 63128
LENGTH: 103
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US-10-449-857A-40

US-10-449-857A-40

SQUENCE 40, Application US/10449857A

PUBLICATION NO. US20040043931A1

GENERAL INFORMATION:

APPLICANT: Hershberg, Robert M.

APPLICANT: Hosken, Nancy A.

APPLICANT: Hosken, Michael J.

APPLICANT: Mohamath, Racdoh

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE

FILE REPREENCE: S84C1

CURRENT APPLICATION NUMBER: US/10/449,857A

CURRENT PILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Corixa Invention Disclosure Database

SQTWARE: Corixa Invention Disclosure Database

LENGTH: 105
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                                                                                                                                                                                                                                               Query Match 100.0%; Score 24; DB 16; Length 98; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49505_1.pep
US-10-767-701-34493
                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C26778_1.pep
US-10-767-701-41212
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COTHER INFORMATION: Unknown Bacterium US-10-449-857A-40
CURRENT FILING DATE: 2004-01-29 WINDER OF SEQ ID NOS: 63128 SEQ ID NO 41212 LENGTH: 98
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Sorghum bicolor
                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
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30 LKAMD 34
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ORGANISM: Unknown
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US-10-767-701-34493
                                                                                                                                                     PEATURE:
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Query Match
Best Local Similarity 100.0%; Score 24; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAWD 5

Db 12 LKAWD 16

Search completed: May 26, 2005, 19:17:35
Job time: 54.8 secs
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14 Page Blank (uspto)

us-10-047-945-3.open.rai

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STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID
HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                US-08-657-163A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Appliseduence 21379, A Sequence 31456, A Sequence 31456, A Sequence 48962, A Sequence 7062, Ap Sequence 8959, Ap
                                                                                26, 2005, 18:29:58 ; Search time 11.4 Seconds (without alignments) 32.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 2
Sequence 4
Sequence 1
Sequence 1
Sequence 2
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    lssued_Patents_AA:*
1: /cgn2_6/ptodata1/liaa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/liaa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/liaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/liaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/liaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/liaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-657-163A-1

US-08-657-163A-1

US-09-252-91A-21179

US-09-270-767-33456

US-09-270-767-48962

US-09-270-767-48962

US-09-270-767-48962

US-09-249-016-11113

US-09-949-016-11113

US-09-949-016-11113

US-09-949-016-11113

US-09-949-016-11113

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US-09-949-016-11113

US-09-949-016-11113

US-09-949-010-1113

US-09-948-010-1113

US-09-968-927-4

US-09-968-927-4

US-09-968-927-4

US-09-968-927-4

US-09-968-927-4

US-09-968-927-4

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US-09-9107-522A-3881

US-07-914-281-14
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US-08-696-731-14
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-092-315-10
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                                                                                                                                                                                                                                                      513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                         US-10-047-945-3
24
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Match Length DB
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Maximum DB &
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                                                                                        Run on:
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No.
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Sequence Seq
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TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTLITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
  JS-09-733-524A-10
JS-09-489-039A-12285
                                                  US-09-600-588-1

US-09-902-1794A-142

US-09-905-125A-142

US-09-902-775A-142

US-09-904-903-603-603

US-09-904-903-142

US-09-904-903-142

US-09-905-381A-142

US-09-905-381A-142

US-09-905-381A-142

US-09-905-381A-142

US-09-905-381A-142

US-09-905-381A-142

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124

US-09-905-381A-124
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ZIP: 77401
COMPUTER READBLE FORM:
COMPUTER: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOPTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FWL-PAT-US-011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08657163A; Patent No. 5744449; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REPERENCE/DOCKET NUMBER: FWI
TELECOMMUNICATION:
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
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ORIGINAL SOURCE: SYNTHETIC

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HAPLOTYPE:
                                 US-08-310-340A-1
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

TITLE OF INVENTION: SYNTHETIC LINES AND THEIR

TITLE OF INVENTION: SYNTHETIC LINES AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES:

ADDRESSEE: BINIE V. LIPPS

STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 24; DB 1; Length 10; 100.0%; Pred. No. 4.2; ive 0; Mismatches 0; Indels
                                                   Length 5;
                                                                                      0; Indels
                                               100.0%; Score 24; DB 1; I 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR NOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/08,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PATTELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                           Sequence 2, Application US/08657163A Patent No. 5744449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: SIN
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Best Local Similarity
Matches 5; Conserv
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US-08-657-163A-3
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Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTLITY AS TREATMENT FOR ENVENOMATION
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INFERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: PLATA AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 18M COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDERF: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE.
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPOSSUM SERA: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORGANISM: DIDELPHIS VIRINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
REPERBUGE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 713-723-6845
                                                                                                                                                                                                                  ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 713-723-68
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18 PRIOR SEQIENCES INVERSE: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: OF SEQIENCES IN 03: 33142 SEQIENCES IN 03: 33142 SEQIENCES IN 03: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33456, Application US/09270767

Sequence 33456, Application US/09270767

Partent No. 6703491

GRNERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 33456

LENGTH: 166
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      AUTHORS: JONAS PERALES, ET AL.

TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLGY
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 4; Length 145; 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 24; DB 4; Length 166; Best Local Similarity 100.0%; Pred. No. 81; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Query Match 100.0%; Score 24; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 6.4; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21379, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT '
ORGANISM: Drosophila melanogaster
US-09-270-767-33456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT;
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 LKAMD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKAMD 5
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US-09-270-767-33456
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                                                              Gaps
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                                                                                                                                                                                                                      DB 1; Length 15;
                                                              0; Indels
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ZIP: 77401
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
COMPUTER: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRAY:
CLONE:
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FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
                                                              Mismatches
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                     100.0%; Score 24; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY AGENT INFORMATION:
NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE/DOCKET NUMBER: FWL-PATTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                  1 LKAMD 5
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Sequence 7062, Application US/09949016

Sequence 7062, Application US/09949016

Beaten No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL 1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PEACESEQ for Windows Version 4.0

SEQ ID NO 7062
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patent No. 681234
patent No. 681239
patent No
                                                                                                                                                                                                                                                                                                                             4; Length 182;
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PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 30086 LENGTH: 182
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US-09-252-991A-30086
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-09-949-016-7062
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US-09-949-016-8959
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER:
US/09/252,991A
CURRENT APPLICATION NUMBER:
US/09/252,991A
PRIOR APPLICATION NUMBER:
US/09/20-18
PRIOR APPLICATION NUMBER:
US/09/20-18
PRIOR FILING DATE:
1998-02-18
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 3226-094
CURRENT APPLICATION NUMBER: 185/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33745
LENGTH: 174
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic 3136-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 48962

LENGTH: 174
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Patent No. 6703491
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; ORGANISM: Drosophila melanogaster
US-09-270-767-33745
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; ORGANISM: Drosophila melanogaster
US-09-270-767-48962
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                        17 LKAMD 21
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Sequence 4560, Application US/09583110

Facent No. 6699703

GENERAL INFORMATION:
FILENGERIAL INFORMATION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE:
FILE REFERENCE:
FILE REFERENCE:
FILE REPERENCE:
FILE REPERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 24; DB 4; I 100.0%; Pred. No. 1.4e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
COMPUTER: <UNKNOWN>
OPERATING SYSTEM: <UNKNOWN>
CURRENT APPLICATION DATA:
FILING DATE: 30-Unn-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/ 085131
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APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4560
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                    111 LKAMD 115
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Redence 25133, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-02-13
FRIOR PILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR SEQ ID NOS: 28208
SEQ ID NO 25133
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11113, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:
FARENT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
THE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 1113
SEQ ID NO 1113
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                                                                                                                                                                                                0; Indels
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ORGANISM: Candida albicans
                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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j TYPE: PRT
j ORGANISM: Human
US-09-949-016-8959
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-949-016-11113
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TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4420:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                     NAME/KEY: misc_feature;
CCATION: (B) LOCATION 1...284;
SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
US-09-107-433-4420
                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMD 5
|||||
60 LKAMD 64
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Search completed: May 26, 2005, 19:08:39 Job time: 12.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 26, 2005, 18:26:23 ; Search time 18:96 Seconds (without alignments) 60.897 Million cell updates/sec

US-10-047-945-4 69 Title: Perfect score:

1 LKAMDPTPPLWI 12 Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	alpha-1-B-glycopro	hypothetical prote	hydroxymethylgluta	TATA-binding prote	hypothetical prote	Ω	fasciclin I precur	immunoglobulin-lik	probable acyl-CoA	lantibiotic Peps b	micofilarial sheat		two-component resp	lipept	probable beta-gluc	probable membrane	dprA protein [impo	gene 65 protein -	hypothetical prote	hypothetical prote	major structural n	beta-galactosidase	protein T24H7.5a [	hypothetical prote	protein T24H7.5b [	rifamycin polyketi		renin (EC 3.4.23.1	hypothetical prote
SUMMARIES	ΩI	A42013	E75099	A31898	A54063	D71194	A81717	A29900	T09402	F86925	S58360	S26854	A40525	C70045	C83867	T02404	\$65208	F87552 ·	831010	T16406	T16659	VHXPMV	A69798	D88175	E70614	C88175	T17466	REMSS	REMSK	C71820
	DB	7	~	-	N	~	7											C3			N	-	Н	~	7	N	~	-	Н	7
	Query Match Length	237	695	932	1213	115	398	662	1327	707	196	205	205	225	406	260	609	365	268	426	492	564	699	1212	1215	1454	1728	401	402	259
di	Query Match	75.4	62.3	62.3	62.3	ö	6.09	ö	6.09	59.4	g)	58.0	58.0	<b>.</b>		•					56.5				Ġ.	•	ė.	•	55.8	55.1
	Score	52	43	43	43	42	42	42	42	41	41	40	40	40	40	40	40	39.5	39	39	39	39	39	39	39	39	39	38.5	æ	38
	Result No.	1	7	m	4	ς.	9	7	œ	σ	10	11	12	13	14	, 15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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Query Match 62.3%; Score 43; DB 2; Length 695; Best Local Similarity 60.0%; Pred. No. 28; Matches 6; Conservative 2; Mismatches 2; Indels

| || ||:|: 561 ANDPKPPMWL 570 3 AMDPTPPLWI 12

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hypothetical prote	peroxidase (EC 1.1	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable nucleopor	steroid hormone re	hypothetical prote	hypothetical prote	hypothetical prote	similar o transcri	hypothetical prote	hypothetical prote		
B70710	T10945	T22794	T29187	C85438	E97580	S62497	805979	T33606	. AB2368	G72520	AE1681	AG2568	A83045	C70829	C87585
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55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	54.3	53.6	53.6	53.6	53.6	53.6	53.6	23.
38 55.1	38 55.1	38 55.1	38 55.1	38 55.1	38 55.1	38 55.1			37 53.6				37 53.6		

# ALIGNMENTS

RESULT 1	
 A42013	
 alpha-1-B-glyco	alpha-1-B-glycoprotein - North American opossum (fragments)
 C;Species: Dide	C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
 C;Date: 10-Jul-	C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
 C;Accession: A42013	2013
 R;Catanese, J.J	.; Kress, L.F.
 Biochemistry 31	Biochemistry 31, 410-418, 1992
 A;Title: Isolat	ion from opossum serum of a metalloproteinase inhibitor homologous to hum
A;Reterence num	A;Reference number: A42013; MUID:92118834; PMID:1731898
 A;Accession: A42013	2013
 A;Status: preliminary	ninary
A; Molecule type: mRNA	: mRNA
A;Residues: 1-237 <cat></cat>	37 <cat></cat>
A, Cross-references: UNIP C, Keywords: glycoprotein	A;Cross-references: UNIPROT:Q28359; GB:J05356 C;Keywords: glycoprotein
Clienty Match	75.4%: Score 52: DB 2: Length 237:
 Best Local Similarity	83.3%; Pred. No. 0.26;
	z; muera o; capa
 0y 1.	1 LKAMDPTPPLWI 12
 	1 LKAMDTTPRLWI 12 .
RESULT 2	
E75099	
hypothetical protein PAR1590	htein DAR1590 - Dyrococcis abyesi (strain Orsay)
C. Coodon Barocoom abinot	occur abitati
C:Date: 20-Aug-	C.bte: 20-Aug-1999 #sequence revision 20-Aug-1999 #text change 09-Jul-2004
C; Accession: E75099	6609
R; anonymous, Genoscope	oscope
submitted to th	submitted to the EMBL Data Library, July 1999
A, Description:	A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001	eer: A/5001
A; Accession: E/5099	
A;Status: preliminary	ninary
A; Molecule type: DNA	DNA .
D-1 : BENDERE CAR	33 SAMIN 34 SAMIN SAMIN CO. MINISTER CO. MIT. SEAEO26. DITM. CADEDO
A; Cioss-Iereren	Afictostices: UNIFROLIGUES: UNIFROLIGUES: UNIFROLIGUES: TION: UNIFROLIGUES: TION: UNDOLOGY NATIONALIST CONTRACTORY NATIONALIST
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A.Generates:	
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Best Local Similarity
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les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: PH1828
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                                                                                                                                                                                                                                                                         A,Reference number: A11898; MUID:89054023; PMID:3192541
A,Recession: A31898
A,Molecule type: mRNA
A,Residues: 1-932 < WOO>
A;Cross-references: UNIPROT:P16393; GB:J04200; NID:g161522; PIDN:AAA30060.1; PID:g161523
A,Note: the authors rearranged portions of the coding region in Figure 2, and the above submitted to GenBank
A;Note: the authors translated the codon GGA for residue 805 as Glu
R;Noodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
J. Biol. Chem. 263, 2513-2517, 1988
A;Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev
A;Recence number: A28367; MUID:88115403; PMID:3276692
A;Accession: A28367
A;Molecule type: mRNA
A;Reference number: A28367; MUID:88115403; PMID:3276692
C;Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t
C;Superfamily: hydroxymethylglutaryl-CoA (HMG-COA) reductase
C;Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N
F;279,850,886,930/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A54063
TATA-Dinding protein-associated factor II - fruit fly (Drosophila melanogaster)
C;Specias: Drosophila melanogaster
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: A54063
R;Verrijzer, C.P.; Yckomori, K.; Chen, J.L.; Tjian, R.
Science 264, 933-941, 1994
A;Title: Drosophila TAP-II 150: similarity to yeast gene TSM-1 and specific binding to C
A;Reference number: A54063; MUID:9423377; PMID:8178153
A;Accession: A54063
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;References: UNIPROT:Q24325; GB:X79243; NID:g541664; PIDN:CAA55830.1; PID:g541665
C;Genetics:
A;Genetics:
A;Genetic
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentro C'Species: Strongylocentrotus purpuratus (purple urchin)
C'Species: Strongylocentrotus purpuratus (purple urchin)
C'Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C'Accession: A31898, A28367
R'Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
Biol. Chem. 263, 18411-18418, 1988
A'Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduc
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hypothetical protein PH1828 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 43; DB 1; Length 932; 70.0%; Pred. No. 38;
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchı DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71194
A;Accession: D71194
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-115 <KAW>
A;Residues: UNIPROT:059492; GB:AP000007; NID:g3236134; PIDN:BAA30947.1; PID:g325
A;Cross-references: UNIPROT:059492; GB:AP000007; NID:g325136134; PIDN:BAA30947.1; PID:g325
A;Experimental source: strain Or3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
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A;Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
A;Experimental source: strain Nigg (MoPn)
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81717
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A; Residues: 1-662 <ZIN>
A; Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
A; Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
R; Snow, P.M.: Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;
Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988
A; Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t
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C;Superfamily: Chlamydia trachomatis hypothetical protein CT036
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2; Mismatches
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Tantiblotic Pep5 blosynthesis protein pep8 - Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S66655; S58360
R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Kem Rimeyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Kem Rimeyer, C.; Biochem. 232, 478-489, 1995
A;Title: Nucleotide sequence of the lantibiotic Pep5 biosynthetic gene cluster and funct A;Reference number: S66651; MUID:96035882; PMID:7556197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Brugia pahangi
C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C;Accession: A46525; S18744
R;Selvik, M.E.; Yazdanbakhsh, M.; Freedman, D.; Blaxter, M.L.; Cookson, E.; Jenkins, R.
J. Bioli Chem. 266, 11002-11008, 1991
A;Title: A proline-rich structural protein of the surface sheath of larval Brugia filari
A;Reference number: A40525; WUID:91250404; PMID:1710216
                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q54123; EMBL: Z49865; NID: 9945014; PIDN: CAA90025.1; PID: 99450
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 826854
R;Selkirk, M
R;Selkirk, Othe EMBL Data Library, February 1991
A;Reference number: 826854
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Pred. No. 23;
1; Mismatches
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Pred. No. 23;
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3; Mismatches
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Pred. No. 8
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milarity 54.5%;
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Best Local Similarity 54.5
Lanes 6; Conservative
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146 LTQQTPTPPIW 156
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-967 <ME2>
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A, Status: preliminary
A, Molecule type: DNA
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F86525
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-707 <STO>
A;Gross-references: UNIPROT:Q9CD82; GB:AL450380; NID:g13092512; PIDN:CAC29642.1; GSPDB:G
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin-like protein IGSF1 - human
immunoglobulin-like protein IGSF1 - human
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C.Accession: T09402
R.Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.
Genomics 48, 157-162, 1998
A.Tile: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.
A.Reference number: Z16665; MUID:98190514; PMID:9521868
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A;Reference number: A94202; MUID:88276943; PMID:2839842
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Pred. No. 61;
2; Mismatches
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Pred. No. 39;
1; Mismatches
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Pred. No. 84;
0; Mismatches
                     A,Accession: A31817
A,Molecule type: mark
A,Residues: 25-42 <SNO>
A,Cross-references: EMBL:M20544; EMBL:J03787
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77.8%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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58.0%; 54.5%;

Query Match Best Local Similarity

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R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul. submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A;Reference number: Z14667
                                                                                                                                                                                                                                                                                                                                      C;Species: Aražidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02404; B84879
                                                                                                                                                                                                                                                                                                                  probable beta-glucosidase homolog F4II.30 - Arabidopsis thaliana
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Cippecies: C70045
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Cippecies: Bacillus subcilis
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Cippecies: C
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R; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4317, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: C83867
A; Status: preliminary
A; Residues: 1-406
A; Residues: 1-406
A; Crosserreferences: UNIPROT:09XC35; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB054
C; Genetics:
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Accession: C83867
       Gaps
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C;Species: Bacillus halodurans
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                                                                                                                                                                                                                                                                                                                                          two-component response regulator [YvqB] homolog yvqA - Bacillus subtilis
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C;Kerwords: phosphoprotein
F;5-113/Domain: response regulator homology <RRH>
F;52/Binding site: phosphate (Asp) (covalent) #status predicted
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Pred. No. 49;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.0%; Score 40; DB 2; Length 225; Best Local Similarity 63.6%; Pred. No. 25; Matches 7; Conservative 1; Mismatches 3; Indels
   4; Indels
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
   6; Conservative
                                                                                                                                               146 LTQQTPTPPIW 156
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                                                                           1 LKAMDPTPPLW 11
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   Matches
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Astatus: translated from GB/EMBL/DDBJ
Astatus: translated from GB/EMBL/DDBJ
Astatus: translated from GB/EMBL/DDBJ
Astatus: translated from GB/EMBL/DDBJ
Astatus: 1-560 cROU>
Astatus: 1-560 cROU>
Astatus: 1-560 cROU>
Astatus: Translation of the content of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2
A;Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 69;
2; Mismatches
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Best Local Similarity 54..
Local 6; Conservative
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A; Residues: 1-560 <STO>
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2005, 18:18:07; Search time 91.68 Seconds (without alignments) 67.026 Million cell updates/sec Run on:

1 LKAMDPTPPLWI 12 US-10-047-945-4 69 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	00++70 4440 35450 3								Q833v1 enterococcu	Q7yqj7 sus scrofa	28bxk6 mus musculu			Q8vm74 rhizobium s		Q9uzg1 pyrococcus				Q7q3z4 anopheles g				Q7wle6 bordetella	Q6yid6 penaeus mon	Q83wx7 streptomyce	P10675 schistocerc	015070 homo sapien	Q8fnb0 corynebacte	kluy	_	Q9w3h5 drosophila
De	100	5	БВ	8	8	8	Ö	0	8	6	8	6	5	8	8	8	P1	8	05	6	8	õ	6	ò	8	8	<u>P</u> 1	2	8	ő	8	8
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% Query Match	000		100.0	87.0	87.0	75.4	72.5	66.7	65.2	65.2	63.8	63.8	62.3	62.3	62.3	62.3	62.3	62.3	60.9	60.9	6.09	60.9	6.09	60.9	6.09	0	6.09	6.09	59.4	59.4	59.4	59.4
Score		0	60	9	9	52	20	46	4.5	45	44	44	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	41	41	41	41
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11,11	Q/mcqs porpnyromon Q8mis3 didelphis m Q8vm3 drosophila	, = 0	•	0			Q00032 brugia paha
Q6UW07 Q9HBJ8	Q7MTQ9 Q8MIS3 Q8VQB3	09CD82 09V0P4	09GZ10	Q54123 Q7KU30	RRPL AHSV9	oeuxuo	Q00032
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# ALIGNMENTS

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Local Similarity
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                  NCBI_TaxID=9267;
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Didelphia lB glycoprotein DVOP51-D (Fragment).
Didelphia marsupialis virginiana (North American opossum).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOP114 (Fragment).
Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
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(Potential).
(Potential).
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-i- PTM: N-glycosylated.
-i- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
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Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX131000; AAN06911.1; -.
                                                                                                                                                                                                                                                                                                                          17A496227E69A65B CRC64;
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(GlcNAc. . .)
(GlcNAc. . .)
(GlcNAc. . .)
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Pred. No. 0.072;
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91.7%;
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Les 12; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                    291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2004 (TrEMBLrel. 26, Last annotation update
Venom metalloproteinase inhibitor DM43b precursor.
                                                                                                                                                                                                                                                                                                                                                                             Score 60; DB 2;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                            InterPro; IPR001559; Ig.
InterPro; IPR001599; Ig.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 291 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY163806; AAN64698.1; -.
HSSP; P24071; 10VZ.
                                                                                                                                                                                                                                                                                                                                                                         87.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.4%;
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                                                                                                   Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the
EMBL; AY131001; AAN06912.1;
HSSP; Q8NHL6; 1GOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Marches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKAMDPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMDPTPRLWI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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314
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5 DPTPPLWI 12
                                                                                                                                                                                                                                                                                                                                                  76 NPTPPLWV 83
                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 128 AA;
                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                              Fraser C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Matches
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                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                        Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL, ASC17233; AASC4008.1; -- Complete protecome.
               Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 2; Length 370;
Pred. No. 37;
                                                                                                                                                     DB 2; Length 227;
                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 2 C2 domains.
                                                                                                                                 227 AA; 24027 MW; 952EA4962C0EE199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40989 MW; C558FDA3D5CD8D8F CRC64;
                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Name=agCG51396; ORFNames=ENSANGG0000014288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0016020; C:membrane; IEA.
GO:0008021; C:synaptic vesicle; IEA.
GO:0005215; F:transporte activity; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                    370 AA
                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                     Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002149; Alatroxin_recept.
InterPro; IPR000008; C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAB01008848; EAA07048.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008973; C2_Calb.
                                                                                                                                                      72.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
         OrderedLocusNames=MAP1691c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; 2.
C2DOMAIN.
                                                                                                                                                     Query Match 72.5
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 54.5
nes 6; Conservative
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146 LAALDPRPPLW 156
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:||| |:|
294 IRALDPTNPIW 304
                                                                                                                                                                                              1 LKAMDPTPPLW 11
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                                                                                                                                                                                                                                                                                                                      AgCP7225 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 AA;
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                                                                    SEQUENCE FROM N.A. STRAIN=k10;
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                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PEST
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                                                                                                                                 SEQUENCE
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Q7QE48;
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Matches
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Q833V1
ID Q833Y
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                                                                                                                                                                   Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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TISSUB=Apical membrane of renal proximal tubule in kidney cortex;

MEDLINE=22753825; PubMed=12740363; DOI=10.1074/jbc.M30320200;

Jutabha P., Kanai Y., Hosoyamada M., Chairoungdua A., Kim D.K.,

Iribe Y., Babu B., Kim J.Y., Anzai N., Chatsudthipong V., Endou H.;

"Identification of a novel voltage-driven organic anion transporter
present at apical membrane of renal proximal tubule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=VS83 / ATCC 700802;
MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 467;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved domain protein.
OrderedLocusNames=EF1825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2%; Score 45; DB 2;
larity 75.0%; Pred. No. 18;
Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 278:27930-27938 (2003).

EMBL; AB104465; BAC76761.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR008957; FN III-like.
InterPro; IPR007114; MFS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis.";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE016952; AA081592.1;
TIGR; EF1825; -.
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1 LKAMDPTPPLWI 12

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128 AA

PRT;

PRELIMINARY;

Q833V1

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
library, clone:B330018M03 product:hypothetical Fibronectin type III
structure containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUE=Adrenal gland; MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUE=Adrenal gland; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Adrenal gland;
Adachi J., Adzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imorani K., Ishii Y., Itoh M., Ragawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=C57BL/621 TISSUE=Adrenal gland;
MEDLINE=C57BL/621 TISSUE=Adrenal gland;
MEDLINE=C57BL/621 FlubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Mishi K., Isohama K., Jagaoka K., Sasahiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishiro T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kachiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                              242 AA
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STRAIN=CS7BL/6J; TISSUE=Adrenal gland;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel, 23,
:||| :||||:
255 IKAMIKSPPLWV 266
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=B930041F14Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                          Q8BXK6
                                                                                                                                                   RESULT 10
                                                                                                                                                                                        Q8BXK(
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Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormBase Consortium;
submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                            Length 242;
                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
Wilson R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The sequence of C. elegans cosmid C25B8.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                     Hypothetical protein.
SEQUENCE 242 AA; 26120 MW; FD8FE24EB994F8F0 CRC64;
                                                                                                                                                                                                                                                                                                                                  .,, AA.
.___2002 (TIENBLEI. 01, Created)
01-MAR-2004 (TIENBLEI. 22, Last sequence update)
Nuclear hormone receptor family protein 120.
Caenorhabditis elegans.
Eukaryota; Meta?~~
Shahai.
                                                                                                                                                                            Score 44; DB 2;
Pred. No. 50;
                                                                                                    MGD; MGI:2444790; B930041F14Rik.
GO; GO:0016021; C:integral to membrane; TAS
                                                                                                                                                                                          Pred. No. 50;
1; Mismatches
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                                                                                                                                                                              63.8%;
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HSSP; P20393; 1A6Y.
                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                       3 AMDPTPPLW 11
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Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
Submitted (JUN-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormBase Consortium;
                                                                                                                                                                                                                                                                   20 AVDPTPPGW
                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                              Query Match
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STRAIN-BR816;
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                                                                                                                                      Query Match
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Q8VM74
                                                                                                                                                                         Best Loc
Matches
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Q846T8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWART; SM00399; ZRF_C4; 1.
PROSITE; PS00011; NUGLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc; Zinc-finger.
SEQUENCE 477 AA; 54900 MW; 9D16A8FF3BDC0241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beginning.";
Genome Res. 6:590-600(1996).
-!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
                 GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005707; F:steroid hormone receptor activity; IEA.

GO; GO:0003700; F:steranscription factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000336; Hrmon_recept_lig.

InterPro; IPR000346; Str ncl_receptor.

InterPro; IPR00124; vitū receptor.

InterPro; IPR001058; Znf_G4steroid.

Pfam; PF00104; Hormone recep; 1.

PRINTS; PR00047; STRDIPINGRR.
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MEDLINE-96389014; PubMed-8796346;
Freiberg C., Perrett X., Broughton W.J., Rosenthal A.;
"Sequencing the 500-kb GG-rich symbictic replicon of Rhizobium sp.
NGR234 using dye terminators and a thermostable 'sequenase': a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium. NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.8%; Score 44; DB 2; Length 477;
54.5%; Pred. No. 1e+02;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-UUL-2004 (Rel. 44, Last annotation update)
Hypothetical 39.2 kDa protein y4vJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 AA
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EMBL, AE000101, AAB91898.1; -.
InterPro, IPR002103, Bac_luciferase.
InterPro, IPR011251; Luciferase_like.
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MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=y4vJ;
Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 54.5
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAMDPTPPLWI 12
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18 KLLHPSPPMWI 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid sym pNGR234a.
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Matches
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ON WAY OF A PROPERTY OF A PROP
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                                                                                                                                                                                                                                                                                                                Gaps
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Pfam; PF00296; Bac luciferase; 1.
Hypothetical protein; Monooxygenase; Oxidoreductase; Plasmid.
SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C88D CRC64;
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Cystobacterineae; Myxococcaceae; Myxococcus.
NCBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBI_TaxID=48291;
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Hartzaell P.L., Youderian P.A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-I.- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-I.- SIMILARITY: Belongs to the peptidase M48 family.
-I.- SIMILARITY: Commentation of the commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.3%; Score 43; DB 2; Length 354; 85.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                            Length 351;
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                                                                                                                                                                                                  Score 43; DB 1; Length 351
Pred. No. 1.1e+02;
1; Mismatches 0; Indele
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical adventurous gliding motility protein M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA
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Rhizobium sp. (strain BR816).
                                                                                                                                                                                                            62.3%;
85.7%;
                                                                                                                                                                                                                                                      Local Similarity 85.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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167 PTPPIWI 173
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STRAIN=GES / OrBay;

MEDLINE=22511545; PubMed=12622808;

Chen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch G., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Cost J., Weissenbach J., Zivanovic Y., Forterre P.;

"An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";

Mol. Microbiol. 47:1495-1512(2003).

EMBL; AJ248266, CAB50098.1; -.

PIR; F57099; E75099.

SEQUENCE 695 AA; 79999 MW; 371E0E402210F551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus abyasi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
                                                                                                                                            Gaps
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GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001915; Peptidase M48.
InterPro; Peptidase M48; I.
Hydrolase; Hypothetical protein; Metalloprotease; Protease; Zinc.
SEQUENCE. 360 AA; 40304 MW; 98AB27E93EAEC023 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                            0
                                                                                                      Query Match 62.3%; Score 43; DB 2; Length 360; Best Local Similarity 66.7%; Pred. No. 1.1e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.3%; Score 43; DB 2; Length 695; Best Local Similarity 60.0%; Pred. No. 2.2e+02; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-UJN-2003 (TYEMBLrel. 24, Last annotation update)
Hypothetical protein.
ORFNames=PAB1590;
                                                                                                                                                                                                                                                                                                    695 AA.
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AMDPTPPLWI 12
                                                                                                                                                                                                            332 MDPEPPRWV 340
                                                                                                                                                                            4 MDPTPPLWI 12
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                                                                                                                                                                                                                                                             RESULT 15
Q9UZG1
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Search completed: May 26, 2005, 18:43:24 Job time : 92.68 secs

| || ||:|: 561 ANDPKPPMWL 570

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model • OM protein Run on:

May 26, 2005, 18:17:22 ; Search time 103.2 Seconds (without alignments) 44.972 Million cell updates/sec

US-10-047-945-4 69 Title: Perfect score:

1 LKAMDPTPPLWI 12 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	ion	Synthetic	N-termina	N-terminu	Synthetic	Synthetic	N-terminu	Synthetic	Synthetic	Enterococ	Novel hum	Novel		Human pro	HMG-COA I	TATA-bind	Drosophi	TATA-bind	Drosophi]	Human	Human	Human	Streptomy	Breast	Human	
,	Description	Abb80225	Aaw11575	Aaw53841	Abb80223	Abb80226	Aaw53843	Abb80222	Abb80227	Adh88053	Abq22890	Abg18144	Abb80228	Aam79784	Adm98800	Aar56496	Aaw06086	Aaw25029	Abb62618	Aao02179	Adb90591	Adb90617	Adh39800	Abr47496	Adp18673	֡
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SUMMAKIES	ID	ABB80225	AAW11575	AAW53841	ABB80223	ABB80226	AAW53843	ABB80222	ABB80227	ADH88053	ABG22890	ABG18144	ABB80228	AAM79784	ADM98800	AAR56496	AAW06086	AAW25029	ABB62618	AA002179	ADB90591	ADB90617	ADH39800	ABR47496	ADP18673	
	DB	7	7	7	7	7	0	7	7	7	4	4	7	4	80	7	ď	~	4	4	7	7	ω	9	œ	
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æ	Query Match	100.0	100.0	100.0	100.0	94.2	78.3	78.3	72.5	65.2	63.8	63.8	62.3	62.3	62.3	62.3	62.3	62.3	62.3	6.09	6.09	6.09	6.09	6.09	6.09	
	Score	69	69	69	69	65	54	54	20	45	44	44	43	43	43	43	43	43	43	42	42	42	42	42	42	
	Result No.	-	7	٣	4	ហ	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Abr12621 Human can Abr12017 Human can Abr12854 Human can Abr12743 Human can	Human Human Human Human		Abr33427 Human can Abr33363 Human can Abb42105 Peptide # Aam75798 Human bon	Aam62985 Human bra Abb40295 Peptide # Aam33978 Peptide #
ABR12621 ABR12017 ABR12854 ABR12743			ABR33427 ABR33363 ABB42105 AAM75798	AAM62985 ABB40295 AAM33978
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228 728 928 9444	2 E E E E E E E E E E E E E E E E E E E		339 440 411 42 41	4443

# ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA. ABB80225 standard; peptide; 12 AA. (first entry) Synthetic LTNF, LT-12. 06-NOV-2003 ABB80225; ABB80225 

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

e.g. Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

Gaps

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Indels

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Pred. No. 0.00041; Mismatches

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12; Conservative

Matches

Best Local Similarity

100.08;

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               Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
                                                                                                                                                                                                                                                                              Gaps
 arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal peptide from lethal toxin neutralising factor.
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                        Score 69; DB 7; I
Pred. No. 0.00033;
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW11575 standard; peptide; 15 AA.
                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                  1 LKAMDPTPPLWI 12
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                                                                                                                                                                                                                                                                                                                1 LKAMDPTPPLWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-011287/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                     Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
20-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW11575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide.
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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                                                                                                                                                                                                                                       LINF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
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100.0%; Pred. No. 0.00041;
ive 0; Mismatches 0;
                                                                                                               AAW53841 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 11; 11pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00058387.
                                                                                                                                                                                                                                                                                               histamine reaction treatment
                                                                                                                                                                                                              N-terminus of opossum LTNF.
                                                                                                                                                                            08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
                    12
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LKAMDPTPPLWI
                                                                                                                                                                                                                                                                                                                            Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipps FW, Lipps BV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                            US5744449-A.
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                                                                                                                                              AAW53841;
                                                                               RESULT 3
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RESULT 4 ABB80223

100.0%; Score 69; DB 2; Length 15

Query Match

(first entry)

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Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin B; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; HDA; asthma; diabetes; autoimmune disease; systemic lugus erythematosus; BIE; rheumatorid arthritis; Gjogren's syndrome; Reiter's syndrome; Paraves' disease; Addison's Alsease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                      14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                   14-JAN-2002; 2002US-00047945
                                             Synthetic LTNF, LT-11.
                                                                                                                                                                                                                                                                                                                                                                            Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-636703/60.
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                                                                                                                                                                                                           WO2003060471-A2
                                                                                                                                                   saliva; ELISA
                                                                                                                                                                                                                                        24-JUL-2003.
                                                                                                                                                                             Synthetic.
                                                                                                                                     Graves'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient
 The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insive growth factor (MGP), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. exythematosus (SLE). Theumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva (collection is relatively non-invasive when compared to blood collection for serum. Saliva proteins
                                                                                                               Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lugue erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assayed by a simple ELISA test, whereas an assay of proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 7; Length 15; Pred. No. 0.00041;
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ABB80223 standard; peptide; 15 AA
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                                                                                                                                                                                                                                                                                                                 14-JAN-2003; 2003WO-US001044.
                                                                                                                                                                                                                                                                                                                                               14-JAN-2002; 2002US-00047945
                                                       (first entry)
                                                                                      Synthetic LTNF, LT-15
                                                                                                                                                                                                                                                                                                                                                                                                                        Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-636703/60.
                                                                                                                                                                                                                                                                                                                                                                           (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                      WO2003060471-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                           saliva; ELISA
                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                    24-JUL-2003
                                                                                                                                                                                                                         Synthetic.
                             ABB80223
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Best Local (
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (19E), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease. Addison's disease or Hodgkin's disease) or depression: The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva can be early election is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             time before centrifugation to separate serum. Saliva proteins ssayed by a simple ELISA test, whereas an assay of proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.2%; Score 65; DB 7; Length 11; 100.0%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assayed by a simple ELISA test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW53843 standard; peptide; 10 AA.
Claim 7; Page 4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKAMDPTPPLW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW53843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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Gaps

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Mismatches

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Conservative 1 LKAMDPTPPLWI 12 

12;

Matches

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Similarity

ABB80226 standard; peptide; 11 AA

ABB80226

ABB80226 ID ABB8 XX AC ABB8 RESULT 5

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (INTR) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (AbA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Siogren's syndrome, Reiter's syndrome, Graves' disease, Adisease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                          Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.3%; Score 54; DB 7; Length 10; 100.0%; Pred. No. 0.067; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80227 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 3; 24pp; English.
                                                                                                                     14-JAN-2003; 2003WO-US001044
                                                                                                                                                                        14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTPPL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic LTNF, LT-9.
                                                                                                                                                                                                                                                                                                 Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                            WPI; 2003-636703/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                    (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                         WO2003060471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                     24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB80227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
ABB80227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometron from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of snake bites, spsis, allergies caused by the environment and treatment of sorptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                           LINF; lethal toxin neutralising factor; opossum; envenomation; therapy, anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; AbA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Siogram syndrome; Reiter's syndrome; Gravee' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(8) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB80222 standard; peptide; 10 AA
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                                                                                                                          histamine reaction treatment
                                                                                                                                                                                                                                                                                                                        96US-00657163
                                                                                                                                                                                                                                                                                                                                                                        93US-00058387
                                                                                                                                                                                                                                                                                                                                                                                                  94US-00310340
N-terminus of opossum LTNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.3
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic LTNF, LT-10.
                                                                                                                                                                      Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-271108/24
                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                        03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                        10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-1994;
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Gaps

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WO2003060471-A2

Synthetic.

saliva; ELISA

ABB80222;

RESULT 7

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Synthetic

patient.

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The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                       New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.2%; Score 45; DB 7; 75.0%; Pred. No. 25;
                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 5938; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 53249; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #22881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG22890 standard; protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SE NPTPPLWV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 DPTPPLWI 12
                                                                                         WPI; 2003-895394/82.
N-PSDB; ADH84648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS87077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 137 AA;
    (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ABG22890
    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (1gB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reliter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                                                                                                        Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis infection; transcription regulatory element;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis polypeptide #2533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH88053 standard; protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 4; 24pp; English.
                                           14-JAN-2003; 2003WO-US001044
                                                                                       14-JAN-2002; 2002US-00047945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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1 LKAMDPTPP 9
                                                                                                                                                                                                 Lipps BV, Lipps FW;
                                                                                                                                                                                                                                            WPI; 2003-636703/60
                                                                                                                                (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6617156-B1
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24-JUL-2003
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Best Loc Matches

ઠ 셤 RESULT 9 ADH88053

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Gaps

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Length 137; 0; Indels

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MPO at the printed specification, but was obtained in electronic format directly from MPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 4; Length 156;
Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #18135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG18144 standard; protein; 303 AA
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed center of the interest of the chain of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80228 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 303 AA;
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (ICMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogran's syndrome, Reiter's syndrome, Graves' disease. Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva centrifugation to separate serum. Saliva proteins collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins can be assayed by a simple ELISA test, whereas an assay of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 43; DB 7; Length 8; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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tao QA, Wang D, Wang
Yang Y, Wejhrman T,
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15-SEP-2000; 2000US-00653551.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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20-JUN-2000; 2000US-00598075.
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
8, Conservative
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Ma Y, Zhao QA,
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
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                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to oytokine, call proliferation or call differentiation or which may induce production of other cytokines in other call propulations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem call growth factor activity, immunoamodulatory activity and activity, tissue growth factor activity, immunoamodulatory activity and activity infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SDD ID NO 2110 (AAK52581), 2111 (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence menceding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.
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                                                                                                                                                                                                                                                                                                                                                      Length 393;
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Pred. No. 1.5e+02;
2; Mismatches 3;
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Claim 20; Page 332; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM98800 standard; protein; 932 AA.
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54.5%;
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Best Local Similarity 54.5.
6; Conservative
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(HART/) HART E A.
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                                                                                                                                                                                                                                                                                                                  Sequence 393 AA;
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                                        conditions where the expression is induced, filtering the cell/resin mixture, extracting the cell/resin mixture, extracting the cell/resin mixture with alcohol to produce an organic eluent and analysing the organic eluent by a screening method including chromatography and/or spectroscopy, to identify the nucleic acid sequence encoding the diterpene synthase. The unicellular microorganism is useful as a diterpene synthase. The unicellular system. Diterpenes, in plants, serve as defence toxins, volatile defensive signals, pollinator attractants and photoprotectants. This sequence the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein associated factor; dTAFISO; screening; diagnostic; gene transcription regulation.
the cells further comprises at least one isolated and purified nucleic acid sequence of a yeast expression library, and the expression of the nucleic acid sequence is regulated by an inducible promoter under
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, useful in screening, diagnostics and therapeutics.
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                                                                                                                                                                                                                                                             Score 43; DB 8; Length 932;
Pred. No. 3.4e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATA-binding protein-associated factor dTAFI50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Arg, Pro or His"
                                                                                                                                                                                                       USPTO at segdata uspto.gov/sequence.html
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1176
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                                                                                                                                                                                                                                                             62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0'
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                                                                                                                                                                                                                                                                                                                                                  298 KKIDPTMPLW 307
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N-PSDB; AAQ70733.
                                                                                                                                                                                                                                     Sequence 932 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang E,
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May 26, 2005, 18:43:39; Search time 78.72 Seconds (without alignments) 52.587 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1462099 segs, 344972447 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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69
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	ption	ence 4, Appli	Sequence 2, Appli	equence 5, Appli	-	6	Sequence 255201,	Sequence 151167,	Sequence 205702,	Sequence 7, Appli	Sequence 168841,	ence 220, App	Sequence 128480,	Sequence 228, App
	Description	Sequ	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Sedu	Segn
	ID	4 US-10-047-945-4	US-10-047-945-2	US-10-047-945-5	US-10-047-945-1	US-10-047-945-6	S US-10-424-599-255201	S US-10-424-599-151167	S US-10-424-599-205702	US-10-047-945-7	. US-10-437-963-168841	S US-10-041-018-220	: US-10-437-963-128480	US-10-177-293-228
	DB	14	14	14	14	14	-	٦	-	14	4	٦	П	٦
	Query Match Length DB	12	15	11	10	0	106	124	144	60	129	932	82	1336
<del>j</del> e	Query Match	100.0	100.0	94.2	78.3	72.5	63.8	63.8	63.8	62.3	62.3	62.3	6.09	60.9
	Score	69	69	65	54	20	44	44	44	43	43	43	42	42
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Sequence 45321, A Sequence 173148, Sequence 253125, Sequence 220724, Sequence 270724, Sequence 2774, App Sequence 387, App	
9 US-09-864-761-45321 15 US-10-424-599-173148 US-10-424-599-223125 15 US-10-424-599-220724 15 US-10-424-599-220724 16 US-10-424-599-179202 17 US-10-424-599-179202 18 US-10-99-179202 19 US-09-989-722-387 10 US-09-989-723-387 10 US-09-989-731-387 10 US-09-989-731-387 10 US-09-991-073-387 10 US-09-991-073-387	ALIGNMENTS
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) OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above. US-10-047-945-4
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        Sequence 4, Application US/10047945
; Publication No. US2003015755A1
; Publication No. US200315755A1
; Publication No. US200315755A1
; Publication No. US200315755A1
; APPLICANT: LIPPS, BRINE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
; TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; TENNEW OF SEQ ID NOS: 7
; SEQ ID NO 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 69; DB 14; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00098; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-047-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 12
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RESULT 2

LKAMDPTPPLWI 12

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ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                         GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: LIPPS, MIDENICATED DISORDERS
FILE REFERENCE: FREDERICK W.
FILE REFERENCE: FREDERICATION OF STATES OF INVENTION: LIPPS, BINELICATION OF STATES OF STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE) IMPLICATED DISORDERS
FILE REPERENCE: FWLPATO15US
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.3%; Score 54;
100.0%; Pred. No.
ative 0; Mismatcl
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SOFTWARE: WORDPERPECT 5.1 FOR WINDOWS
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
OTHER INFORMATION: SYNTHESIZED.
OTHER INFORMATION: US 5,576,297.
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US-10-047-945-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
US20030157555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
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Best Local Similarity
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US-10-047-945-5
US-10-047-945-5
Sequence 5, Application US/10047945
Fublication No. US2003015755A1
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E;
TITLE OF INVENTION: (1gE) IMPLICATED DISORDERS
FILE REPERENCE: FWLD-AD15US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR FILING DATE:
PRIOR FILING DATE:
                Sequence 2, Application US/10047945
Publication No. US2003015755541
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOCLOBULIN E FILE REPERENCE: FWLPATO15US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT PILING DATE: 2002-01-14
PRIOR FILING DATE:
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100.0%; Score 69; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.2%; Score 65; DB 14;
100.0%; Pred. No. 0.0036;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT S.1 FOR WINDOWS
SEQ ID NO SEA LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: SYNTHESIZED. OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic. US-10-047-945-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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Best Local Similarity
Matches 11; Conserv
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LENGTH: 15
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Gaps

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15; Length 144;

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corresponds to fragment 1-8 of 2 above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10047945
; Beblication No. US20030157555A1
; GENERAL INPORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (1gB) IMPLICATED DISORDERS
; FILE REFERRINCE: FWLPATOLISU
; CURRENT FILING DATE: 2002-01-14
; PRIOR PILING DATE: 2002-01-14
; ROUPHER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.3%; Score 43; DB 14; Length 8; 100.0%; Pred. No. 1.3e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_2777C.1.pep
US-10-424-599-205702
                                                                                                                                                                                                      LOCATION: (1)..(144)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                   DB
56;
                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 168841, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                      63.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic.
US-10-047-945-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                     NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205702
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 85.7
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.3
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                             TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PTPPLWI 12
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1 LKAMDPTP 8
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APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cavalua APPLICANTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255201
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151167, Application US/10424599
; Bublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AND APPLICANT: AND APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 151167
LENGTH: 124
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Anoust Thomas J
APPLICANT: Anoust Thua
APPLICANT: Canoust Thua
APPLICANT: Canoust Thua
APPLICANT: Canous Thua
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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85.7%; Pred. No. 42;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.8%; Score 44; DB 15; Length 124; 75.0%; Pred. No. 49; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107527C.1.pep
US-10-424-599-151167
                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201
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Best Local Similarity 75.0°
Then 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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92 PTPPLWV 98
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US-10-424-599-151167
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Indels

Length 82;

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; OTHER INFORMATION: Clone ID: PAT_MRT4530_30829C.1.pep US-10-437-963-128480
                                                                             Score 42; DB 16;
Pred. No. 66;
1; Mismatches 1
                                                                                                                                                                                                                                                                                             Sequence 228, Application US/10177293 Publication No. US20030124128A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bast Jr., Robert C.
Hortobagyi, Gabriel N
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                                           Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                           60.9%;
                                                                               Query Match 60.9
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myer, Vic
Wang, Youzhen
                                                                                                                                                                                                                                                                                                                 Publication LC. GENERAL INFORMATION:
APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MDPTPPLWI 12
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     FEATURE:
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Fublication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: LA ROSS, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Brarbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5)321)B

CURRENT APPLICANT: APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966
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| Sequence 220, Application US/10041018
| Publication No. US20040072323A1
| GENERAL INFORMATION:
| APPLICANT: Matsuda, Selichi P.T.
| APPLICANT: Hart, Elizabeth A.
| TITLE OF INVENTION: Diterpne-Producing Unicellular Organism FILE REFERENCE: POLOGOUS1/10025547
| CURRENT APPLICATION NUMBER: US/10/041,018
| PRIOR APPLICATION NUMBER: US/10/041,018
| PRIOR APPLICATION NUMBER: US 60/259880
| PRIOR FILING DATE: 2001-01-05
| NUMBER OF SEQ ID NOS: 413
| SEQ ID NO 220
| LENGTH: 932
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                                                                                                                                                                                                                   Length 129;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_67316C.1.pep
US-10-437-963-168841
                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                             Score 43; DB 16;
Pred. No. 71;
                                                                                                                                                                                                                                                       1; Mismatches
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168841
LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Strongylocentrotus purpuratus US-10-041-018-220
                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0
Matches : 7; Conservative
                                                                                                                                                                                                                                                                                             1 LKAMDPTPPLW 11
                                                                                                                                                                                                                                                                                                                                 84 LARMPPSPPLW 94
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298 KKIDPTMPLW 307
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ORGANISM: Oryza sativa
                                                                                                                   ORGANISM: Oryza sativa
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LENGTH: 82
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APPLICANT: Sahin, Aysegual
APPLICANT: Sahin, Aysegual
APPLICANT: Sahin, Aysegual
APPLICANT: Sahin, Aysegual
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, MILLS, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MR.-038
CURRENT PAPLICATION NUMBER: US/10/17,293
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-27
PRIOR PELING DATE: 2001-06-27
PRIOR PELING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-03-25
PRIOR PELING DATE: 2002-03-05
PRIOR PELING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
NUMBER OF SEQ ID NOS: 506
NUMBER PERSON PROSESSOR
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Best Local Similarity 77.8%; Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-864-761-45321
; Sequence 45321, Application US/09864761
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LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AL133458.11

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68

OTHER INFORMATION: SWISSEROT HIT: O53951, EVALUE 6.40e+00

OTHER INFORMATION: EST_HUMAN HIT: A1986481.1, EVALUE 6.00e-16

US-09-864-761-45321
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                                                                                                                                                                                                                                                                                                                       | TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROAL CURRENT APPLICATION NUMBER: US/09/864,761
| CURRENT PILING DATE: 2001-05-23
| PRIOR APPLICATION NUMBER: US 60/180,312
| PRIOR APPLICATION NUMBER: US 60/207,456
| PRIOR APPLICATION NUMBER: US 60/203,665
| PRIOR PILING DATE: 2000-05-26
| PRIOR PILING DATE: 2000-06-36
| PRIOR PILING DATE: 2000-10-04
| PRIOR PILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-
US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Gaps ; 0

> 2 KAMDPTPPLWI 12 KSMGPAPPRWM 15

> 유 ઠ

US-10-424-599-173148

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Experiment David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173148
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_127369C.1.pep
US-10-424-599-173148
Sequence 173148, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 26, 2005, 19:17:48
Job time : 91.72 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.4%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DPTPPLW 11
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Sequence

Sequence 178, App Sequence 13655, A Sequence 15934, A

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Sequence 1, Application US/08310340A

Sequence 1, Application US/08310340A

Patent No. 5576297

GENERAL INFORMATION:

TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

NUMBER OF SEQUENCES: 1

CORRESPONDENCE BINIE V. LIPPS

STREET: 4509 MINGSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

STATE: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: MS FORD S. 0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,340A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION UNDERER: 08/058,387

FILING DATE: 10 MAY 1993

NAME: NAME:

NAME:

NAME:

NAME:

NAME:

NAME:

TITLE OF INVENTATION:

SACTION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993
US-09-134-000C-6583
US-09-252-991A-30473
US-08-311-731A-216
US-09-540-236-3413
US-09-270-767-42895
US-08-439-009A-5
US-08-439-009A-5
US-09-370-700-5
US-09-370-700-5
US-09-248-796A-25521
US-09-248-796A-25521
US-09-248-796A-25521
US-09-249-076-7
US-09-989-703-7
US-09-989-703-7
US-09-989-703-7
US-09-989-703-7
US-09-989-703-7
US-09-247-155-178
US-09-247-155-178
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRINIANA
STRAIN: WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15
 TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                      US-08-310-340A-1
 Sequence 1, Appli
Sequence 2, Appli
Sequence 5938, Ap
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 43223, A
Sequence 67545, A
Sequence 8760, Ap
Sequence 18, Appl
Sequence 18, Appl
Sequence 42265, A
Sequence 18, Appl
Sequence 42265, A
Sequence 42265, A
Sequence 18, Appl
Sequence 42265, A
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444, App
444, App
21988, A
41296, A
56512, A
26963, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43480,
                                                                                                        May 26, 2005, 18:29:58; Search time 27.36 Seconds (without alignments) 32.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 4
Sequence 4
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-657-163A-1

US-08-657-163A-1

US-08-657-163A-1

US-08-6134-000C-5938

US-09-134-000C-5938

US-09-134-000C-5938

US-09-186-58-20

US-08-64-715-20

US-09-270-767-57545

US-09-270-767-57545

US-09-270-767-57545

US-09-949-016-876

US-09-949-016-876

US-09-949-016-876

US-09-949-016-876

US-09-949-016-876

US-09-949-016-876

US-09-977-2685-44

US-09-902-540-16548

US-09-500-124-444

US-09-500-124-444

US-09-270-767-56512

US-09-270-767-56512

US-09-270-767-56512

US-09-270-767-56512

US-09-270-767-56512

US-09-270-767-56512

US-09-270-767-5480

US-09-071-035-230

US-09-071-035-230

US-09-11-035-230

US-09-11-035-230
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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69
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Match Length
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SEQUENCE CHARACTERISTICS:
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Patent No. 574449

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MINOSA DR.
CITT: BELLAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: JOUNG PERALLES, ET AL.
TITLE: ANTI-SNAEVE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 69; DB 1; I
100.0%; Pred. No. 6.4e-05;
tive 0; Mismatches 0;
                 DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL INE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBBRAY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: DELLARIES

STATE: TEXAS

ZIP: 77401

ZIP: 77401

COMPUTER READALLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: BM COMPATIBLE
OCNERATING SYSTEM: MS-DOS 5.0/MINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION NUMBER: 08/058,387
ATTORNEY AGENT 1NFORMATION: STATORNEY AGENT NUMBER: 28,198
REGISTRATION NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
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Matches 12; Conservative
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TELEFAX: 713-663-7290
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INDIVIDUAL ISOLATE:
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STEADLE STROLE
STEADLE TYPE: 10 FOOTEN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-LERISE: NO
ANTI-L
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1 LKAMDPTPPLWI 12
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
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Sequence 5938, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lyun Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

SPIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE PATENTING DATE: 1377

LENGTH: 137
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Batent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wisegand, Roger C.
APPLICANT: Wixegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.3%; Score 54; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAX 1993
ATTORNEY/ABGNT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
RESPERNCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecalis US-09-134-000C-5938
                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                               TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKAMDPTPPL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-134-000C-5938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-657-163A-2
                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hoey, --
APPLICANT: Ruppert, Siegitiec.
APPLICANT: Ruppert, Siegitiec.
APPLICANT: Tanee, Macko
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                               Score 43; DB 4; Length 397; Pred. No. 33; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELS PC-COMPATIBLE
COMPUTER: TBM PC-COMPATIBLE
COMPUTER: TBM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILLNG DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
MAMBE: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                   62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 781-1989
                                                                                                                                                        TYPE: PRT // ORGANISM: Myxococcus xanthus US-09-902-540-13316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1213 amino acids
                                                                                                                                                                                                                                                 Query Match 62.3
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       369 MDPEPPRWV 377
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Gaps

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GENERAL INFORMATION:
APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE ON INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 42265
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57545
LENGTH: 198
                                                                                                                                                                                                                                                                                    Query Match 59.4%; Score 41; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 43; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.0%; Score 40; DB 4; Length 360; Best Local Similarity 54.5%; Pred. No. 91; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 4;
Pred. No. 48;
3; Mismatches
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                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-57545
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; Sequence 57545, Application US/09270767
; Patent No. 6703491
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US-09-270-767-42265
Sequence 42265, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Drosophila melanogaster
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ORGANISM: Drosophila melanogaster
                                                                                                                                                         ORGANISM: Drosophila melanogaster
     CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5%;
Matches 6, Conservative 3
                          NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43223
LENGTH: 253
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70 IKAVSPSPNLW 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                  43 MDPTPPL 49
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                                                                                                                                      TYPE: PRT
                                                                                                                                                                                      FEATURE:
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                      APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Huppert, Brian D.
APPLICANT: Huppert, Siegfried
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
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Pred. No. 1.1e+02;
1; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PPC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 37,7239
INFORMATION FOR SEQ ID NO: 20:
COMPUTED SEQ ID NO: 20:
                                                                                                                                                      Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%;
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LENGTH: 1213 amino acids
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620 LSAMDDSPVLWI 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-646-715-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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Length 198; 2; Indels ö

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TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
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Matches 6; Conservative
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134 KSDDPTNPIW 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-477-396A-18
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US-07-857-224B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                       ; GENERAL INFORMATION: TO Craig et al.

J APPLICANT: VENTER, J., Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PELICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRACESEQ for Windows Version 4.0

SEQ ID NO 8760
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US-08-477-396A-18
Sequence 18, Application US/08477396A
Fatent No. 5872235
GENERAL INFORMATION:
APPLICANT: Chen, Lan Bo
APPLICANT: Liu, Yuan
FITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
TITLE OF INVENTION: 1 SOLATING SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,396A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%; Score 39; DB 75.0%; Pred. No. 24; ive 1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,488
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: US 08/448,388
FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12502
                                                                                                                                                                                                                                    Sequence 8760, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.v
6; Conservative
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CITY: Boston
STATE: Massachusetts
COINTRY: USA
                                       :||: |:| ||
70 IKAVSPSPNLW 80
1 LKAMDPTPPLW
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61 RTMDPTPP 68
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                    US-09-949-016-8760
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US-09-270-767-45215
US-09-270-767-45215
Sequence 45215, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 3326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45215
LENGTH: 210
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Patent No. 5958784
GENERAL INFORMATION:
APPLICAMT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: none-
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 4; Length 210;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 2;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
FILING DATE: 31-OCT-1994

ATTORNEY AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346

REFERENCE/DOCKET NUMBER: DFCI-333BX
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-229

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Drosophila melanogaster US-09-270-767-45215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%;
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US-09-902-540-16548

| Sequence 16548, Application US/09902540
| Sequence 16548, Application US/09902540
| Patent No. 633447|
| GENERAL INFORMATION:
| APPLICANT: Goldman, Barry S. APPLICANT: Glater, Steven C. APPLICANT: Wiegand, Roger C. APPLICANT: WIEGANG: 38-10(15849)B
| CURRENT APPLICATION NUMBER: 60/217,883 |
| PRIOR APPLICATION NUMBER: 60/217,883 |
| PRIOR FILING DATE: 2000-07-10 |
| WINDER OF SEQ ID NOS: 16825 |
| SEQ ID NO 16548 |
| LENGTH: 557 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
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COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFFICATION: 436
PRIOR APPLICATION DATA: none
TELEPHONE: (International) 41 1 262 2437
TELEFAX: (International) 41 1 262 2437
TELEFAX: none
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH 267 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPDLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKAMDPTPPL 10
|| :||| |
31 LKVVDPTPEL 40
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5 DPTPPLWI 12 :|||| |: 135 EPTPPHWL 142

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Search completed: May 26, 2005, 19:08:40 Job time : 28.56 secs

Tue May 31 05:58:12 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

May 26, 2005, 18:26:23 ; Search time 12.64 Seconds (without alignments) 60.897 Million cell updates/sec

US-10-047-945-7 43 Title: Perfect score:

1 LKAMDPTP 8 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	hypothetical prote	~	protein kinase (EC	protein kinase (EC	kinase	kinase	protein kinase raf	,×,	ribosomal protein	hypothetical prote	protein-glutamine	protein kinase raf	protein-glutamine	DNA-binding protei	tryptophan synthas	probable transport	hypothetical prote	protein-glutamine	internalin like pr	2-isopropylmalate	protein-glutamine	protein-glutamine	protein-glutamine	protein-glutamine	protein-glutamine	granulocyte colony		granulocyte colony	similar o transcri
SUMMAKIES	ΙD	T29187	A42013	TVMVF6	TVFVMM	TVRTRR	S00644	TVHUF6	TVRTRF	G64225	E87327	PD0001	TVXLRF	A29996	A34203	E64679	AB3370	AF2070	A44302	AG1598	140725	JC5133	B39045	A39045	S19680	A47203	B38252	JH0329	C38252	AE1681
	DB	7	N	Н	Н	~	Н	Н	Н	~	~	~	-	Н	7	~	~	~	7	7	7	7	-	Н	~	П	7	~	7	7
	Query Match Length	792	237	323	380	602	647	648	648	66	350	444	638	691	2717	262	408	416	548	620	638	680	687	. 687	687	698	771	783	863	142
de	Query Match	88.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	79.1	76.7	76.7	76.7	76.7	76.7	× 74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	72.1
	Score	38	35	35	35	35	35	35	35	34	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	31
	Result No.	П	7	М	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote probable oxidoredu	carbonyl reductase carbonyl reductase	catechol 1,2-dioxy hypothetical prote	probable glycohydr hypothetical prote	alpha-2-HS-glycopr countertrypin prec	hypothetical prote fetuin precursor -	probable fibrillin conserved hypothet	hypothetical prote
T16668 T37152	JC5285 JC5284	JC6206 T21569	T36869 T49597	S21094 JC5431	G87706 . A32827	C84769	T33287 T17332
01 02	0 0	0 0	0 0	0 0	0 0	01 0	0 00
180 253	276	285 323	339 339	345 348	361	376	431
72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1
31 31	31	31	31	31	31	3.3	31
30 31	33	9 9 4 6	36 37	3 3 3 3	440	4. 4 2. £	4 4 4 7

### ALIGNMENTS

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A;Gene: CESP:C55C3.3
A;Map position: 4
A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43
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hypothetical protein C55C3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Tae. 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 (C;Accession: T29187 th. Woessne, J; Stellyes, L. submitted to the EMBL Data Library, April 1996 A;Beferance number: Z20585 A;Accession: T29187 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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### 133 LKPMDPTP 140 œ 1 LKAMDPTP ò 셤

alpha-1-B-glycoprotein - North American opossum (fragments)
C;Species: Didelphis virginiana, Didelphis mareupialis virginiana (North American opossu C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
R;Catanese, J.J; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum A;Reference number: A42013; MUID:92118834; PMID:1731898 A, Cross-references: UNIPROT: 028359; GB: J05356 C; Keywords: glycoprotein A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-237 <CAT>

Gaps ö Score 35; DB 2; Length 237; Pred. No. 11; 0; Mismatches 1; Indels Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative C

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1 LKAMDPTP

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Gaps

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C; Superfamily: Kinase-related transforming protein; protein kinase homology C; Superfamily: ATP; oncogene; phosphotransferase; polyprotein; serine/threonine-specific px R; 80-346/Romain: protein kinase homology <KIN> P; 88-96/Region: protein kinase ATP-binding motif F; 88-96/Region: protein kinase ATP-binding motif F; 108/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-rC;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: B26126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: rat protein kinase raf; protein kinase homology
C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon;
C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon;
F; 301-57/Domain: protein kinase homology KIN>
F; 309-317/Region: protein kinase ATP-binding motif
F; 329/Active site: Lys #status predicted
F; 453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase raf-1 (EC 2.7.1.-) - chicken
NyAlternate names: kinase-related transforming protein raf-1; mht/raf; protein kinase c-
C;Species: Gallus Gallus (chicken)
C;Date: 18-Oct-1989 #sequence revision 23-Aug-1996 #text_change 09-Jul-2004
C;Accession: S00644; I50380; I50381
C;Accession: M.; Sippel, A.E.; Trachmann, C.; Bister, K.
Oncogene 2, 179-185, 1988
A;Title: Primary structure of the chicken c-mil protein: identification of domains share
A;Reference number: S00644; MUID:88217299; PMID:3285296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P05625; EMBL:X07017; NID:g63232; PIDN:CAA30069.1; PID:g63233: R;Flordellis, C.S.; Kan, N.C.; Lautenberger, J.A.; Samuel, K.P.; Garon, C.F.; Papas, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RjIshikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A;Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A;Reference number: A26126; MUID:87172791; PMID:3550433
    A;Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, A;Reference number: A21137; MUID:84221892; PMID:6328485
A;Accession: A21137
                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-210,'B','212-230,'B',232-380 <KA2>
A;Cross-references: GB:KO2082
C;Comment: This protein is translated as a gag-mht or gag-mil polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-602 <1SH>
A;Cross-references: GB:M15428; NID:g206546; PIDN:AAA42002.1; PID:g206547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 380
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Pred. No. 20;
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110 LKVVDPTP 117
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A; Residues: 1-647 < KOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTP
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NyAlternate names: kinase-related transforming protein mil (mht); mil proto-oncogene pro CiSpecies: avian myelocytomatosis virus MH2

NyAlternate names: kinase-related transforming protein mil (mht); mil proto-oncogene pro CiSpecies: avian myelocytomatosis virus MH2

A;Note: host Gallus gallus (chicken)

C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C;Accession: A00639; B00638; A21137

R;Sutrave, P: Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Bister, K.

Nature 309, 85-88, 1984

A;Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine ret
A;Reference number: A00639

A;Molecule type: DNA

A;References: UNIPROT: P00531; GB: K02082

A;Note: the authors translated the codon CAG for residue 58 as Gly

R;Kan, N.C.; Flordellis, C.S.; Mark, G.B.; Duesberg, P.H.; Papas, T.S.

S;ience 223, 813-816, 1984

A;Reference number: A00639; MUID: 84121298; PMID: 6320371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: kinase-related transforming protein; protein kinase homology | Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase; 322-286 Domain: protein kinase homology «KIN» | 330-38 Region: protein kinase ATP-binding motif | 550/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A00638; A38020
C;Accession: A00638; A38020
C;Accession: A00638; A38020
A;Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin A;Reference number: A00638; MUD:84121298; PMID:6320371
A;Reference number: A00638
A;Reference number: A00638
A;Residues: 1-323 < KANA
A;Cross-references: UNIPROT:P00532
A;Residues: 1-323 < KANA
A;Cross-references: UNIPROT:P00532
A;Reference number: A30020
A;Reference number: A30020; MUD:84172180; PMID:6324342
A;Reference number: A30020
A;Molecule type: DNA
A;Residues: 1-323 < KANA
A;Residues: 1-323 < KANA
A;Cross-reference number: A30020
A;Molecule type: DNA
A;Residues: 1-323 < KANA
A;Residues: 1-333 < KANA
A;Residues: 1-333 < KANA
A;Residues: 1-333 < KANA
A;Residue
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                                                                                                                                                                                                                                                                  rotein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-
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R;Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984
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                                                                                                                                                                                                                                                                                                                                                                   Species: murine sarcoma virus 3611
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A;Molecule type: DNA
A;Residues: 1-210,'E',212-380 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: host Mus musculus (mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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LKVVDPTP
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Score 35; DB 1;
Pred. No. 36;
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6; Conservative
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                                                          AyRestence number: 190380

AyRestence: 200-30 cFLO.

AyRestence: 200-30 cFLO.

AyCology 143, 35-36-36.

AyRestence: 200-316.

AyRestence: 150381

AyRestence: 150381

AyRestence: 150381

AyRestence: 150381

AyRestence: 150381

AyRestence: 200-318.

AyRestence: 200-31
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NyAlternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene protein kinase protein kinase (EC 2.7.1.37)
C; Specise: Homo aspiens (man)
C; Specise: Homo aspiens (man)
C; Specise: Homo aspiens (man)
C; Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C; Accession: A00637; IS7580
R; Bonner, T.I.; Oppermann, H.; Seeburg, P.; Kerby, S.B.; Gunnell, M.A.; Young, A.C.; Rag Nucleic Acids Res. 14, 1009-1015, 1986
A; Title: The complete coding sequence of the human raf oncogene and the corresponding st A; Reference number: A00637; MUID:86120351; PMID:3003687
A; Molecule type: mRNA
A; Residues: 1.648 cBON1>
A; Molecule type: mRNA
A; Residues: 1.648 cBON1>
A; Molecule type: mRNA
A; Residues: 1.548 cBON1>
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Title: Structure and biological activity of human homologs of the raf/mil oncogene.
A; Residues: 228-239, L., 241-541, I', 143-648 cBON2>
A; Steatus: translated from GB/EMBL/DDBJ
A; Cross-references: GB:L00212; NID:g190837; PIDN:AAA60247.1; PID:g496091
R; Morrison, D.K.; Heidecker, G.; Rapp, U.R.; Copeland, T.D.
J. Biol. Chem. 268, 17309-17316, 1993
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fitle: Analysis of the cellular proto-oncogene mht/raf: Relationship to the Reference number: 150380; MUID:86098644; PMID:3002017
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A; Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept A; Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept A; Pathway: MAP kinase cascade
C; Superfamaliy: protein kinase A-raf; protein; phosphorotein; phosphorransferase; proto-oncogenc P; 139-184/Domain: protein kinase C zinc-binding repeat homology «KZN»
F; 135-184/Domain: protein kinase C zinc-binding repeat homology «KZN»
F; 135-362/Region: protein kinase APP-binding motif F; 139-165, 168, 184/Binding site: phosphate (Ser) (Covalent) #status experimental
F; 139, 165, 168, 184/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F; 139, 165, 176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F; 159, 165, 176/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status experimental
F; 168, 188, Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experimental
F; 1899/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F; 1899/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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N;Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
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Cross-references: UNIPROT:P11345; GB:M15427; NID:g206544; PIDN:AAA42001.1; PID:g206545
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A, Note: expression is ubiquitous in mammalian tissues that have been studied
C, Superfamil: protein kinase A-raf; protein Kinase C zinc-binding repeat homology; prot
C, Keywords: AFP; autophosphorylation; phosphoprotein; phosphorransferase; proto-oncogene
F;139-184/Domain: protein kinase C zinc-binding metif
F;355-363/Region: protein kinase ATP-binding metif
F;355/Rinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;259/Rinding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
F;499/Rinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;499/Rinding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
F;499/Rinding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
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JBhikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Ol. Cell. Biol. 7, 1226-1232, 1987
JILle: Rat c-raf oncogene activation by a rearrangement that produces a fused protein seference number: A26126; MUID:87172791; PMID:3550433
                                                                                                                                                                            have been studied
kinase C and other kinases,
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A; Title: Identification of the major phosphorylation sites of the Raf-1 kinase. A; Reference number: A43089; MUID: 93352516; PMID: 8349614
A; Contents: annotation; phosphorylation sites
A; Note: expression is ubiquitous in mammalian tissues that have been studied
C; Comment: After phosphorylation and activation by protein kinase C and other k
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3p25-3p25
A;Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3;
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Pred. No. 36;
1; Mismatches
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Length 648;

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Tue May 31

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R;Ikura, K.; Nasu, T.; Yokota, H.; Sasaki, R.; Chiba, H.
Agric. Biol. Chem. 51, 957-961, 1987
A;Title: Cloning of cDNA coding for guinea pig liver transglutaminase.
A;Reference number: PD0001
                                                                                                                                                                                                                     C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: aminoacyltransferase
F;89/Active site: Cys #status predicted
                                                                                                                                                                                               A; Cross-references: UNIPROT: Q7M0F8
                                                                                                                                                                                                                                                                                                                   76.7%;
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Matches 5; Conservative
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167 VQALDPTP 174
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                                                                                                                            A; Status: preliminary A; Molecule type: mRNA
                                                                                                     A; Accession: PD0001
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A; Title: The minimal gene complement of Mycoplasma genitalium.
A; Reference number: A64205
A; Reference number: A64205
A; Reseasion: G64225
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-99 < TIGR>
A; Residues: 1-99 < TIGR>
A; Conetic code: SGC3
C; Genetic code: SGC3
C; Superfamily: hypothetical protein ysxB
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Cispecies: Caulobacter crescentus
Cipate: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
CiAccession: E87327
RiNierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Lamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Dodson, R.J.; Canin, M.L.; Haft, D.H.; Kolon
I. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Felerence number: A87249; MUID:21173698; PMID:11259647
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A,Residues: 1-350 <STO>
A,Cross-references: UNIPROT:Q9AAG8; GB:AE005673; NID:g13421843; PIDN:AAK22617.1; GSPDB:G
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Species: Mycoplasma genitalium
Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
       Gaps
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46;
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    6; Conservative
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60 LKLIDPTP 67
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protein kinase raf-1 (EC 2.7.1.-) - African clawed frog
M.Alternate names: Kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: 801930; ISI254
R;le Guellec, R.; le Guellec, K.; Paris, J.; Philippe, M.
Nucleic Acids Res. 16, 10357, 1988
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A; Residues: 1-638 -LEGS.
A; Residues: 1-638 -LEGS.
A; Cross-references: UNIPROT: P09560; EMBL: X12948; NID: g65027; PIDN: CAA31407.1; PID: g65028;
R; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Paris, J.; Le Fur, N.; Philippe, M.
Biol. Cell 72, 39-45, 1991
A; Title: Xenopus c-raf proto-oncogene: cloning and expression during oogenesis and early
A; Reference number: 151254; MUID: 92096753; PMID: 1721855
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A;Cross-references: GB:S74063; NID:g241259; PIDN:AAB20707.1; PID:g241260
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Length 444;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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Score 33; DB 2
Pred. No. 61;
3; Mismatches
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198 LKAFSPTP 205
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                                             protein-glutamine gamma-glutamyltransferase (BC 2.3.2.13) - guinea pig protein-glutamine gamma-glutamyltransferase (BC 2.3.2.13) - guinea pig C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Accession: A29996
R;Ikura, K.; Nasu, T.; Yokota, H.; Tsuchiya, Y.; Sasaki, R.; Chiba, H.
Biochemistry 27, 2898-2905, 1988
A;Title: Amino acid sequence of guinea pig liver transglutaminase from its cDNA sequence A;Reference number: A29996; MUID:88294033; PMID:2900023
A;Accession: A2996
A;Accession: A2996
A;Accession: A2996
A;Accession: A2996
A;Accession: Diver
A;Experimental source: liver
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: aminocyltransferase
F;277/Active site: Cys #status predicted
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A Residues: 1-2717 <FAN>
A Cross-references: UNITAROT: P15822; EMBL: X51435; NID: 938017; PIDN: CAA35798.1; PID: 938018
R; Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
MOI. Cell. Biol. 10, 1406-1414, 1990
MOI. Cell. Biol. 10, 1406-1414, 1990
A; Title: A large protein containing zinc finger domains binds to related sequence elemen A; Reference number: A34779; MUID: 90205817; PMID: 2108316
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A;Molecule type: mRNA
A;Residues: 801-1072,'N',1074-1168,'K',1170-1225,'V',1227-1434,'N',1436-1607,'I',1609-16
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NiAlternate names: major histocompatibility complex enhancer-binding protein 1

Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004

C;Accession: A34203; A34779

E;Fan, C.M.; Maniatis, T.

Genes Dev. 4, 29-42, 1990

A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that A;Reference number: A34203; MUID:90169514; PMID:2106471
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64679
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C,Superfamily: HIV-EP2 enhancer-binding protein
C,Keywords: DNA binding; transcription regulation; zinc finger
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A; Status: preliminary
A; Molecule type: mRNA
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUD:97394467; PMID:9252185

A;Accession: E64679

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-262 <TOM>
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A;Cross-references: UNIPROT:P56141; GB:AE000612; GB:AE000511; NID:92314443; PIDN:AAD0832 C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology F;17-244/Domain: tryptophan synthase alpha chain homology <TRPA>

Gaps ö Query Match 74.4%; Score 32; DB 2; Length 262; Best Local Similarity 75.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 2; Indels

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                                       May 26, 2005, 18:18:07; Search time 61.12 Seconds (without alignments) 67.026 Million cell updates/sec
                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                               Q95qq6
Q19055
Q807x3
Q807x3
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Q67624
P00532
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Q015278
Q99058
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Q99059
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Q6C847
Q6C847
O91725
O91902
Q902h8
Q758i7
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Q43221
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08p816
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                                                                                                                                      1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                        1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                            RAFI_CHICK
RAFI_HUMAN
RAFI_MOUSE
RAFI_MAU
V233_MYCGE
06CS47
091725
091725
091726
075817
075817
075817
078187
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Q8HZ75

DM43
 DDMR
Q8HZ74

Q95QG6
019055
Q9CU36
Q8HXX5
Q8HXX5
Q8HXX5
Q8AFXX6
Q67624
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Maximum Match 100%
Listing first 45 summaries
                            protein search, using sw model
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Q15278
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Q8P816
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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                                                                                     1 LKAMDPTP 8
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                                                                                                                                                        bacillus
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SEQUENCE 17 AA; 1947 MW; CB55F840B73B2A2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
NCBI_TaxID=9267;
                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                 Didelphis.
           Q82y16
Q81kf6
Q9deb2
Q9y3g7
Q9y3g7
Q9aag8
Q91t12
Q7mui8
Q63c05
Q61h70
Q61h70
Q61h70
  28pjg8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B 91ycoprotein DVOP51-D (Fragment).
Didelphis marsupialis virginiana (North American opossum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; Length 17;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY131000; AAN06911.1; -.
HSSP; 076036; 10LL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15297 MW; E19D071A76AA5A7F CRC64;
                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 13, Last sequence update)
ANTI-BOTHROPIC complex 48,000 SUBUINT (Fragment).
Didelphis marsupialis (Southern opossum).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Didelphimorphia; Didelphidae;
NUSI TAXID=9268;
                                                                                                                                                                                                                                                      17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                           ALIGNMENTS
Q8PJG8
PCN2 PYRAE
Q8LKF6
Q9DEB2
                                                                                                                                                                                                                                                                             Created)
                                            Q8Y3G7
Q9M3Z4
Q9AAG8
Q91T12
Q7MU18
Q63C05
Q6NH70
Q813N0
                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                        Q6HJF9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
8; Conservative
 2009
2256
2256
2350
3342
3375
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3375
                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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76.71
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SEQUENCE
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                               Q9TR78;
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                                                                                                                                                                                                                              RESULT 1
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8; Conservative
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Submitted (SEP-2004)
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STRAIN-Bristol N2;
WormBase Consortium;
                                                                                                                                                                                                                                                             1 LKAMDPTP 8
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                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                 SEQUENCE FROM N.A.
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                                                                                                                                                                        SEQUENCE
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095006;
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            Gaps
                                                                                                                             16-OCT-2001 (Rel. 40, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
05-UTU-2004 (Rel. 44, Last annotation update)
Venom metalloproteinase inhibitor DM43.
Velos marsuplails (Southern opossum)
Didelphis marsuplails (Southern opossum)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1B glycoprotein DVOPIL4 (Fragment).
Didelphis marsuplalis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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(Potential).
(Potential).
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                                                                                                                                                                                                                                                  MEDLINE=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
                                                                                                                                                                                                                                                                                                                                                                     NOTE-Ref.1.
-!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
InterPro; IPR007110; Ig-like.
InterPro; IPR011015; LEM_like.
                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Homodimer.
-!- TISSUB SPECIFICITY:
-!- PTH: N-glycosylated:
-!- PTH: N-glycosylated:
-!- MASS SPECIROMETRY: MW-42691; METHOD=MALDI; RANGE=1-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; Length 291;
Pred. No. 2.5;
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32390 MW; 17A496227E69A65B CRC64;
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(GlcNAc...)
(GlcNAc...)
(GlcNAc...)
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Ig-like V-type 1.
Ig-like V-type 2.
Ig-like V-type 3.
Potential.
 Pred. No. 1.1;
                                                                                                           291 AA
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           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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N-linked
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                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY.
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 100.08;
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           8; Conservative
                                                                                                           STANDARD;
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                                                     42 LKAMDPTP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AA;
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Best Local Similarity
Matches 8; Conserv
Best Local Similarity
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                                                                                                                                                                                                          NCBI_TaxID=9268;
                                                                                                           DIDMR
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                                                                                    RESULT 3
DM43_DIDMR
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           Matches
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08HZ74
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AC 08HZ
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
NCBI_TaxID=9267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length 291;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                             Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AN131001; AN066912.1; -.
HSSP; Q8NH6; 1GOX.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; I.
SWART; SW00409; IG; I.
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STRAIN-Bristol N2;
Woessne J., Stellyss L.;
"The sequence of C. elegans cosmid C55C3.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C55C3.6.
Name=C55C3.6; ORFNames=C55C3.6;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mandiyan S., Schumacher C., Cioffi C., Sharif H., Yuryev A., Lappe Monia B., Hanson S., Goff S., Wennogle L.P.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AF006463; AAB63196.1; -.
HSSP; P54763; 1JPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:000554; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyroaine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00179; Frot Kinase.
InterPro; IPR00179; For kinase.
InterPro; IPR00179; Frot kinase.
InterPro; IPR00179; Tyr pkinase.
PF00069; Pkinase: 1.
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                                                                                                                                          2; Length 274;
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                                                                                                                                                                             1; Indels
  (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                11 protein.
274 AA; 30019 MW; D7EAE6046588BDA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AA; 34230 MW; 3512983ADF5D1A3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0109; TYRKINASE.
Prodom; PD000001; Proc kinase; 1.
PROSITE; PS001017; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 AA.
                                                                                                                                      88.4%; Score 38; DB
87.5%; Pred. No. 24;
iive 0; Mismatches
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Submitted (SEP-2004) to the EMBL/Gs
EMBL; U53335; AAL2732.1; -.
WormBase; WBGene00016956; C55C3.6.
WormPep; C55C3.6; CE29736.
Hypothetical protein.
SEQUENCE 274 AA; 30019 MW; D7E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, (TrEMBLrel. 17, I
                                                                                                                         Query Match
Best Local Similarity 87.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-RAF homolog (Fragment).
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                             133 LKPMDPTP 140
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LKVVDPTP 37
                                                                                                                                                                                                                    1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
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01-JUN-2001 (
01-JUN-2001 (
01-MAR-2004 (
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09CU36
1D 09CU;
AC 09CU;
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DT 01-JI
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[1]
SEQUENCE FROM N.A.
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Q85453;
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085453

10 085455

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Trugillo M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C., Domont G.B., Ho.P.L., Perales J., Domont G.B., Ho.P.L., Perales J., Bubmitted (CCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX163806; AAN64698.1; -...
HSSP, P24071; 1007.2
InterPro; IPR0073599; Ig.
InterPro; IPR007110; Ig-like.
Ffam; PF00047; ig; 1.
PR081T; SM00409; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 314 venom metalloproteinase inhibitor DM43b
314 AA, 34604 MW, 69D55F54486D35A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last asequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Venom metalloproteinase inhibitor DM43b precursor.
Didelphia marsuplails (Southern opossum).
Budaryota, Metazoa; Chordara; Craniata; Vertebrata; Buteleostomi; Mammalia; Metatheria; Didelphiae; Didelphis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 35; DB 2; Length 308; 75.0%; Pred. No. 1.1e+02; ive 1; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase transforming protein raf (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                    308 AA; 35058 MW; F87DD6ABE27600BB CRC64;
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004572; F:protein binding; IPI.
GO; GO:0004672; F:protein binding; IPI.
GO; GO:0004724; P:protein kinase activity; TAS.
GO; GO:0007243; P:protein kinase cascade; TAS.
InterPro; IPR000719; Prot kinase ...
InterPro; IPR008271; Ser Thr pkin AS.
ProDom; PD00009; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN I.
PROSITE; PS00108; PROTEIN KINASE DOM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LKVVDPTP 44
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Matches 6; Conserv
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P00532;
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RAF_MSV36
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DT 21-JU
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DE GEC 2
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
3611 raf gene. (Fragment).
Murine sarcoma virus.
Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
Murine sarcoma virus 1611.
Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
NCBL_TaxID=11812;
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS001108; PROTEIN KINASE ST; 1.
ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
                                                                                                     [1] -
SEQUENCE FROM N.A.
MEDLINE=84121298; PubMed=6320371;
MEDLINE=84121298; PubMed=6320371;
MEDNINE=84121298; PubMed=6320371;
MA common onc gene sequence transduced by avian carcinoma virus MH2
"A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyprotein. SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- MISCELLANEOUS: This protein is synthesized as a Gag-Raf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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MEDINE=84172180; PubMed=6324342;
Mark G.E., Rapp U.R.;
"Primary structure of v-raf: relatedness to the src family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (By similarity).
ATP (By similarity).
Pszboron acceptor (By similarity).
Fszbs423A66E362F3 CRC64;
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PIR; A00638; TVMVF6.
HSSP; P54763; 1JPA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser Thr pkin AS.
Pfam; PP00069; Pkinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 224:285-289(1984)
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LKVVDPTP 59
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Best Local Similarity
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subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
MEDLINE=84121298; PubMed=6320371; Ran N.C., Flordellis C.S., Mark G.E.; Duesberg P.H., Papas T.S., M. Common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
NON TER
                                                                                                 GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004648; P:protein-agricase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00171; Ser thr pkin AS.
InterPro; IPR00271; Ser thr pkin AS.
InterPro; IPR00271; Ser thr pkin AS.
InterPro; PR000269; Tyr pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.4%; Score 35; DB 2; Length 359; 75.0%; Pred. No. 1.3e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AA; 40935 MW; 5B6C615C5331570D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
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NCBI_TaxID=36381;
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InterPro; IPR011009; Kinase_like.
InterPro; IPR000719; Protc Kinase.
InterPro; IPR008916; Retrov_capsid_C.
InterPro; IPR008911; Ser_thr_pkin_AS.
Pfam; PF002093; Gag_D30; I.
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LKVVDPTP 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=6328485;
Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
"Nucleotide sequence of avian carcinoma virus MH2: two potential onc
genes, one related to avian virus MC29 and the other related to murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: By itself the v-Mil oncogene has only weak transforming capacity but it abolishes the growth factor requirements of avian macrophages transformed by other oncogenes.
-!- CATALYTIC ACTIVITY: A protein = ADP + a phosphoprotein.
-!- MISCELLANEOUS: This protein is synthesized as a Gag-Mht or Gag-Mil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-84121298; PubMed-6320371; Kan N.C., Flordellia C.S., Mark G.E., Duesberg P.H., Papas T.S.; M.Z. common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611.";
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine,threonine-protein kinase; Transferase.
SEQUENCE 375 AA; 42459 WW; 7FB38ESC5866DD99 CRC64;
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SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAF
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                                                                                               Length 375;
                                                                                                                                                                                                                                                                                                                           P00531;
21-UU-1986 (Rel. 01, Created)
21-UU-1986 (Rel. 01, Last sequence update)
25-CUT-2004 (Rel. 45, Last annotation update)
Serine/threonine-protein kinase transforming protein mil
                                                                                                                                   1; Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
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                                                                                             Score 35; DB 2; I
Pred. No. 1.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                             380 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine retroviral oncogene v-raf.";
Nature 309:85-88(1984).
                                                                                                                                                                                                                                                                                                             PRT;
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PIR; A00639; TVFVNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84191511; PubMed=6325930;
                                                                                             h 81.4%;
Similarity 75.0%;
6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 2.7.1.37).
Name=V-MIL; Synonyms=V-MHT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 223:813-816(1984)
                                                                                                                                                                                                                                                                                                           STANDARD;
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LKVVDPTP 112
                                                                                                                                                                         1 LKAMDPTP 8
                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
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1 LKAMDPTP 8
                     Query Match
Best Local Similarity
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Bonner T.I., Kerby S.B., Sutrave P., Gunnell M.A., Mark G., Rapp U.R.;
"Structure and biological activity of human homologs of the raf/mil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Proc kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MO1. Cell. Biol. 5:1400-1407(1985).

-1 - SIMILARITY: Belongs to the Ser/Thr protein kinase family.

R EMBL; L00212; AAA60247.1; -.

R EMBL; L00206; AAA60247.1; JOINED.

R EMBL; L00209; AAA60247.1; JOINED.

R EMBL; L00209; AAA60247.1; JOINED.

R EMBL; L00213; AAA60247.1; JOINED.

R PRF; S60341; S60341.
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                                                                                                                           Protein kinase.

ATP (By similarity).

ATP (By similarity).

Proton acceptor (By similarity).

G -> E (in Ref. 3).

6498695FB7EBEESD CRC64;
                                                                                                                                                                                                                                                  Score 35; DB 1; Length 380; Pred. No. 1.4e+02; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA.
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                                                                                                                          82 341 Pr.
88 96 ATI
108 108 AT
201 201 Pr.
211 211 G
380 AA; 42853 MW;
                                                                                                                                                                                                                                                    81.4%;
75.0%;
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Query Match
Best Local Similarity 75.vv,
Bernaga 6; Conservative
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Name=RAF1;
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110 LKVVDPTP 117
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                                                                                                                                                                                                                                                                                                                         1 LKAMDPTP 8
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                                                                                                             Transferase.
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CONFLICT
SEQUENCE
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BINDING
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MEDLINE=21481893; PubMed=11597136; DOI=10.1006/geno.2001.6627;
Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;
Gray T.A. onservation of the makorin-2 gene, encoding a multiple zinc-finger protein, antisense to the RAF1 proto-oncogene.";
Genomics 77:119-126(2001).
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MGD; MGI:97847; Rafi.

MGD; MGI:9005829; C:Cytosol; TAS.

MGC; GO:0005829; C:Cytosol; TAS.

MGC; GO:0005815; F:protein binding; IPI.

MGC; GO:0007219; P:protein kinase activity; TAS.

MGC; GO:0007219; DAG_PE-bind.

MICEPPO; IPRO00719; Prote kinase activity; TAS.

MICEPPO; IPRO00719; Prote kinase.

MICEPPO; IPRO00719; Prote kinase.

MICEPPO; IPRO00719; Prote kinase.

MICEPPO; IPRO0081; Prote kinase; 1.

MR Pfam; Pro0130; C11; 1.

MR Pfam; Pro130; PRO008; DAGPEDOMAIN.

MR Pro200; DAGPEDOMAIN.

MR PROSITE; PRO0109; C1; 1.

MR PROSITE; PSO0109; C1; 1.

MR PROSITE; PSO0109; MINASE ATP; UNKNOWN.

MR PROSITE; PSO0109; RIDAG_PE BIND DOM_2; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RIDAG_PE BIND DOM_1; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RIDAG_PE BIND COM_2; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RADEIN KINASE_ST; 1.

MR PROSITE; PSO0109; RIDAG_PE BIND COM_2; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RIDAG_PE BIND COM_2; 1.

MR PROSITE; PSO0109; RIDAG_PE BIND COM_2; 1.

MR PROSITE; PSO0109; RRD; 1.

MR PROSITE; PSO0109; RRD; 1.
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                                                                        Gaps
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01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-077-2003 (TrEMBLrel. 17, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Protein kinase raf 1 (Fragment).
Name=Raf1; Synonyms=cRAF;
Name=Raf1; Synonyms=cRAF;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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SEQUENCE FROM N.A.
TISSUB-Liver;
TOIS N., Abe S.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
HSSP; P11345; 1RRB.
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Score 35; DB 2; Length 421;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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75.0%; Pred. No. 1.9e+02;
tive 1; Mismatches 1;
                                                                        1; Mismatches
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   81.4%;
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nes 6; Conservative
                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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150 LKVVDPTP 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                         1 LKAMDPTP
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Search completed: May 26, 2005, 18:43:27 Job time : 64.12 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May Run on:

26, 2005, 18:17:22 ; Search time 68.8 Seconds (without alignments) 44.972 Million cell updates/sec

US-10-047-945-7 score: Perfect

1 LKAMDPTP 8 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg 0B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp1980s:* geneseqp1990s:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

## SUMMARIES

		J			SOMERTES		
Result No.	Score	Query Match	Length	DB	ID	Description	
, ,	43	100.0	8	7	ABB80228	Abb80228 Synthetic	
7	43	100.0	6	7	ABB80227	Abb80227 Synthetic	
e	43	100.0	10	7	AAW53843	Aaw53843 N-terminu	
4	43	100.0	10	7	ABB80222	Abb80222 Synthetic	
S	43	100.0	11	7	ABB80226	Abb80226 Synthetic	
9	43	100.0	12	7	ABB80225	Abb80225 Synthetic	
7	43	100.0	15	7	AAW11575	Aaw11575 N-termina	
œ	43	100.0	15	~	AAW53841	Aaw53841 N-terminu	
σ	43	100.0	15	7	ABB80223	Abb80223 Synthetic	
10	35	81.4	29	Н	AAP81131	Aap81131 c-raf-rel	
11	35	81.4	94	4	AAO02179	Aao02179 Human pol	
12	35	81.4	267	7	AAY43943	Aay43943 Yeast pro	
13	35	81.4	344	2	ADF18626	Adf18626 Protein c	
14	35	81.4	405	7	AB062609	Abo62609 Klebsiell	
15	35	81.4	615	9	ABU08102	Abu08102 Human kin	
16	35	81.4	615	œ	ABM82924	Abm82924 Human dia	
17	35	81.4	648	7	AAR22560	Aar22560 Mouse mut	
18	35	81.4	648	~	AAR22562	Aar22562 Mouse mut	
19	35	81.4	648	~	AAR22563	Aar22563 Mouse mut	
20	35	81.4	648	7	AAR25277	Aar25277 Human c-r	
21	35	81.4		~	AAR22561	Aar22561 Mouse mut	
22	35	81.4	64	~	AAR22559	Aar22559 Mouse c-r	
23	35	81.4	648	~	AAR98215	Aar98215 Human Raf	
24	35	81.4	648	N	AAW13107	Aaw13107 Human Raf	
25	35	81.4	648	7	AAW17048	Aaw17048 Mutant mo	

648 2 AAW17047 648 2 AAW17044 648 2 AAW17045 648 2 AAW17046 648 2 AAW17049 648 2 AAW3066 648 2 AAW3066 648 2 AAW3066 648 2 AAW3066 648 2 AAW30667 648 2 AAW30667 648 3 AAB42701 648 3 AAB42701 648 4 AAB70295 648 4 AAB70295	242		Aay08981 Human c-R Aaw30668 Mutant mo Aaw30666 Mutant mo	Human Mutan Mouse	Human Human Amino	Aag67619 Amino aci Aab70295 Human c-R Aag67440 Amino aci
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	AAW17047 AAW17044 AAW17045	AAW17046 AAW17049 AAW62220 AAW95611	AAY08981 AAW30668 AAW30666	AAW30664 AAW30667 AAW30665	AAY94501 AAB42701 AAB08773	AAG67619 AAB70295 AAG67440
	548 548 548 548 2	2222	00000	2000		8 8 8 4 4 4
	81.4 81.4 81.4	81.4 81.4 81.4 81.4	81.4 81.4 4.1.6	811.4 811.4 81.4	81.4 81.4 81.4	81.4 81.4 81.4
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3323	3 2 2 2	3333	2 2 2 2 2	3 3 3	333
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	26 27 28	33 32 32	33 34 33 4 45 45 45 45 45 45 45 45 45 45 45 45 45	. B. B. B. C. B. C	0 4 4 0 1 2 5	44 44 5

## ALIGNMENTS

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; ABB80228 standard; peptide; 8 AA. 06-NOV-2003 (first entry) Synthetic LINF, LT-8. ABB80228; 

saliva; ELISA.

Synthetic.

WO2003060471-A2.

24-JUL-2003.

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

Lipps BV, Lipps FW;

WPI; 2003-636703/60.

Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

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arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection of serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type ELISA
         88888888888888888
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Sequence 8 AA;

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Gaps
                                ;
           Length 8;
                               0; Indels
          100.0%; Score 43; DB 7; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
Query Match
Quest Local Similarity 100.00
Echag 8; Conservative
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ABB80227 standard; peptide; 9 AA
        06-NOV-2003
     ABB80227;
RESULT 2
 ABB802
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Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; Synthetic LINF, LT-9

saliva; ELISA

Synthetic.

WO2003060471-A2

24-JUL-2003

14-JAN-2003; 2003WO-US001044.

14-JAN-2002; 2002US-00047945.

(LIPP/) LIPPS B V. (LIPP/) LIPPS F W.

WPI; 2003-636703/60.

Lipps BV, Lipps FW;

e. Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a patient

Claim 7; Page 4; 24pp; English.

The sequences given in ABB8022-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by

Sequence 10 AA;

to horse

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenometion from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
performing an enzyme-linked immunosorbent assay (BLISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins serum requires a more complicated sandwich type BLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                               100.0%; Score 43; DB 7; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                AAW53843 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-00058387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00657163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminus of opossum LINF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Didelphis virginiana.
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х х
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                           1 LKAMDPTP
                                                                                                                                                                                                                                                        LKAMDPTP
                                                                                                                                                Sequence 9 AA;
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(LIPP/) LIPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1993;
22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5744449-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAW53843;
                                                                                                                                                                                 Query Match
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenobiles (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, atthritis, Siogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva canfine lesing an anti-serum that is specific for the protein. Saliva can be centrifiged immediately, whereas blood requires
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                                                                                                                                                                                                                                                                                                                                            Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clotting time before centrifugation to separate serum. Saliva proteins
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                     ö
                   Length 10;
                                                     0; Indels
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                 100.0%; Score 43; DB 2; 100.0%; Pred. No. 0.16;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assayed by a simple ELISA test
                                                                                                                                                                                                        ABB80222 standard; peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                            (first entry)
                                                     Conservative
                                                                                                                                                                                                                                                                                                               Synthetic LTNF, LT-10
Query Match
Best Local Similarity
8; Conserv?
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                                                                                                     LKAMDPTP
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                                                                                     1 LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   saliva; ELISA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgB levels, e.g. asthma, c.g. diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease.

Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme dimmunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection collection are the protein and protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ABA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
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                                                                                                                                                                                                       ABB80226 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-2002; 2002US-00047945.
                                                                                                                                                                                                                                                                                                                      06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic LTNF, LT-11.
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                                       1 LKAMDPTP
LKAMDPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  saliva; ELISA
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                                                                                                                                                                                                                                                                  ABB80226;
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Gaps

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Indels

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Mismatches

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Conservative

1 LKAMDPTP

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Gaps

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100.0%; Score 43; DB 7; Length 10; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels

8; Conservative

Query Match Best Local Similarity Matches 8; Conserv

100.08;

Query Match Best Local Similarity 8; Conserve

100.0%; Score 43; DB 7; Length 11; 100.0%; Pred. No. 0.18;

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthitis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease, or depression; The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires collecting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                         Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 43; DB 7; Length 12;
; Pred. No. 0.2;
0; Mismatches 0; Indels
                                                                                               ABB80225 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 4; 24pp; English.
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Similarity 100.0%;
8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2003; 2003WO-US001044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2002; 2002US-00047945
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                              Synthetic LTNF, LT-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipps BV, Lipps FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-636703/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003060471-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
                                                                                                                                                                        06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                    ABB80225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patient.
                                                       RESULT ABB8022
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The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTMF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTMF and the 15mer peptide against venom from snakes of the families Crotalidae, Blaphidae, Hydrolidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
                                                                                                                                                              Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 43; DB 2; Length 15; 100.0%; Pred. No. 0.25; cive 0; Mismatches 0; Indels
                                                                                                                                  N-terminal peptide from lethal toxin neutralising factor.
                  AAW11575 standard, peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53841 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                     94US-00310340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Col 9; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                    93US-00058387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminus of opossum LTNF.
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                    (revised)
                                                                                                                                                                                                                  Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipps FW, Lipps BV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-011287/01.
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                                                                                                                                                                                                                                                                                                                                                                                  (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                  22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                    LO-MAY-1993;
                                                                                25-MAR-2003
20-MAR-1997
                                                                                                                                                                                                                                                    US5576297-A.
                                                                                                                                                                                                                                                                                     19-NOV-1996.
                                                 AAW11575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW53841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide.
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AAW11575
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AAP81131 standard; protein; 29 AA
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                14-JAN-2002; 2002US-00047945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87EP-00109985.
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                         Lipps BV, Lipps FW;
                                                                                                                      WPI; 2003-636703/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                           (LIPP/) LIPPS B V. (LIPP/) LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-1986;
10-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1990
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01-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3P253325-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 8
                                                                                                                                                                                                   patient
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                                                                                                                                                                                                                                                                                                                                                               This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNP) moiety from a 68 kba anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Blapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of be or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; 1GE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression;

    can neutralise

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                                                                                                                                                                                                                                                                                        Lethal Toxin Neutralising Factor peptide from opossum venom(s) from all major families of poisonous snakes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80223 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 11; 11pp; English.
                                                                                                                                 93US-00058387.
94US-00310340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2003; 2003WO-US001044.
                                                                                                      96US-00657163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic LTNF, LT-15.
           Didelphis virginiana.
                                                                                                                                                                                                                              Lipps BV;
                                                                                                                                                                                                                                                           WPI; 1998-271108/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKAMDPTP 8
                                                                                                                                                                                LIPPS B V.
LIPPS F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          horse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003060471-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
                                                                                                                                                                              (LIPP/) LIPPS
(LIPP/) LIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baliva; ELISA
                                                                                                      03-JUN-1996;
                                                                                                                                   10-MAY-1993;
                                                                                                                                                   22-SEP-1994;
                                         US5744449-A.
                                                                        28-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-2003
                                                                                                                                                                                                                             Lipps FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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ABB80223;

RESULT 9

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The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTMF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (MGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva centralinged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins
                                                                  e.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be assayed by a simple ELISA test, whereas an assay of proteins from
serum requires a more complicated sandwich type ELISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing asthma or diabetes, by employing an ELISA on a saliva sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 43; DB 7; Length 15; 100.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncogene related peptide; c-raf-related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-raf-related peptide c-raf-1 (142-170)
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Sequences ANY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as interaction of a protein with other molecules
this patent did not form part
ined in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
inflammation. Note: The sequence data for this patent did not of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2; Length 267;
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
                                                                                                                                  Length 94
                                                                                                                                                                           Indels
                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting the folded structure of proteins.
                                                                                                                               Score 35; DB 4
Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 225-228; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                             AAY43943 standard; protein; 267 AA.
                                                                                                                                  81.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00857224
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast protein kinase #10.
                                                                                                                                                        Local Similarity 75.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                    48 LKSODPTP
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                                                                                                                                                                                                                        1 LKAMDPTP
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                                                                                           Sequence 94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BENN/) BENNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAY43943;
                                                                                                                                    Query Match
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynpeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                    One of 3 c-raf-1-related peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                    New oncogene related peptide(s) - useful in prepn. of antigen and then antibodies having specific reactivity with cancer proteins.
                                                                                                                                                                                                                        among 23 claimed oncogene-related peptides. See also AAP81114-30 and AAP81132-P81134. (Updated on 01-JUL-2002 to add missing PI field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                        81.4%; Score 35; DB 1; Length 29; 75.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                    solid phase or soln. methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 16071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA002179 standard; protein; 94 AA.
                                                                                                                                                        Claim 19; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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LKVVDPTP 16
    Yanaihara N;
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                                             WPI; 1988-015700/03
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LKAMDPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI82110.
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                                                                                                                                                                                                                                                                                                               Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
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Homo sapiens.

07-SEP-2001

Tang YT,

06-NOV-2001

AAO02179;

RESULT 11

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Gaps

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Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                  N-PSDB; ACH96160
                                                                                                                                                                                                                                                                                                                                                                              Sequence 405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003012065-A2
                                                                                                                  29-JAN-1999;
                                               JS6610836-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                      26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2003
                                                                                                                                                                Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU08102;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of protein c-Raf-1 (amino acids 305-648). Human papillomavirus oncoprotein B7 abrogates Raf-associated arrest and prevents inhibition of cyclin E-CDK2 activity without disrupting Raf induction of p21Cip21. B7 neither interacts with p21Cip1 nor derepresses p21Cip1-associated CDK2 activity, but instead reduces the association between p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steadystate levels of Akt, a regulator of p21Cip1 localisation, leading to loss of p21Cip1 phosphorylation and accumulation of p21Cip1. B7 disrupts the effects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. Maintenance of Akt activity is necessary and sufficient to bypass Raf arrest. The invention provides methods for identifying and using inhibitors of B7 cell proliferation activity, and for identifying and using unhibitors of B7 cell proliferation activity, and for identifying and using the methods can be used to inhibit aberrant cellular proliferation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                            Identifying a compound that inhibits B7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                  Human; c-Raf-1; oncoprotein E7; p21CIP1; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant expression vector; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 7; Length 344;
Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klebsiella pneumoniae polypeptide seqid 9126.
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2; 119pp; English.
                      ADF18626 standard; protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO62609 standard; protein; 405 AA.
                                                                                                                                                                                                            21-APR-2003; 2003WO-US012667
                                                                                                                                                                                                                                   19-APR-2002; 2002US-0374245P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.08;
                                                                                           Protein c-Raf-1 (aa305-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 75.v»,
6; Conservative
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                               Mccance D, Westbrook TF;
                                                                                                                                                                                                                                                        (UYRP ) UNIV ROCHESTER
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LKVVDPTP 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer.
                                                                                                                                                                                                                                                                                                      WPI; 2003-845498/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 344 AA;
                                                                                                                                                              WO2003088922-A2
                                                                                                                                        Homo sapiens
                                                                    12-FEB-2004
                                                                                                                                                                                     30-OCT-2003.
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                                             ADF18626;
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                                                                                                                                                                                                                                                                                                                                                                  activity
RESULT 13
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ID ABO6
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AC ABO6
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DT 29-J
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KW Recx
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New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a new isolated nucleic acid encoding a Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regularory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; enzyme; kinase and phosphatase; KPP; cancer; cirrhosis; cell proliferative disorder; arteriosclerosis; atherosclerosis; procythamia to accordance in the semalatis; polycythamia vera; psoriasis; primary thromobocytopaenia; developmental disorder; renal tubular acidosis; anental retardation; AIDS; epilepsy; neurological disorder; Alzheimer's disease; Parkinson's disease; autoimmune disorder; inflammatory disorder; allergy; asthma; acquired immunodeficiency syndrome, autoimmune thyroiditis; contact dermatitis; Crohn's disease; diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease; glomerulonephritis; Goodpasture's syndrome; multiple sclerosis; osteoprosals; panceathis; Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human kinase and phosphatase protein, KPP-3, INCYTE No.6464221CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 9126; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                    27-JAN-2000; 2000US-00489039.
                                                                                                                                                                                                                                                                                                                   99US-0117747P.
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75.0%;
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hes 6; Conservative
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Klebsiella pneumoniae
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186 IKARDPTP 193
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The invention relates to an isolated polypeptide, which is a human kinase and phosphatase, KPP (KPP-1 to KPP-1B). Also included are the encoding polymuclectides KPP NA, recombinant polymuclectide comprising a promoter sequence operably linked to KPP NA, a cell transformed with the
                                                                                                                                                                                                                          New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                Claim 1; Page 159-160; 199pp; English.
                             07-AUG-2001; 2001US-0310393P.
09-AUG-2001; 2001US-0311323P.
07-SEP-2001; 2001US-0317820P.
14-SEP-2001; 2001US-0322264P.
28-SEP-2001; 2001US-032264P.
19-DEC-2001; 2001US-0332009P.
                                                                                                                                                 Yue H, Walia NK,
Lal PG, Elliott
, Richardson TW,
01-AUG-2002; 2002WO-US024521
                      2001US-0309627P
                                                                                               2002US-0364494P
                                                                                                        24-APR-2002; 2002US-0375539P
                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                           WPI; 2003-239519/23.
                                                                                                                                                                                                       N-PSDB; ABX13149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 615 AA;
                                                                                                                                                  Baughn MR, Yue
Gietzen KJ, La
Emerling BM, 1
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recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an anti-KPP antibody, screening for anti-KPP antibody, screening for anti-KPP antibody, screening for cantidonists of KRP, screening for compounds which bind to or alter the activity or expression of KPP, microarray where at least one element is KPP NA, generating an expression profile of a sample containing for capturity or expression of KPP, microarray where at least one element is polymucleotides and an array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate (where at least one of the nucleotide molecules comprises a first oligonucleotide or polymucleotides of a target KPP NA). The kinases and phosphatases or plymucleotides, polymucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal concurnal heamoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopaenia or cancer), developmental disorders (renal tubular acidosis, anaemia or mental retadation), neurological disorders (e.g. Alzheimer's disease, parkinson's disease or palleysy), autoimmune (c.g. Alzheimer's disease, parkinson's disease or palleysy), autoimmune (c.g. Alzheimer's disease, parkinson's disease or palleysy), autoimmune (c.g. Alzheimer's disease, disease, parkinson's disease or palleysy), autoimmune (c.g. Alzheimer's disease, disease, disease, date (c.g. AlDS), acquired immunodeficiency syndrome, altergies, asthma, autoimmune thyroiditis, irritable bowel syndrome, disease, disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarchritis, Sjogren's syndrome, remarcial disease Hashimoto's thyroiditis, pancreatitis, parcetilal parasitic, protozoan or helminthic infections. They are also useful in the assessment of the effects of exogenic animals to model human disease. T

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0; Gaps
   81.4%; Score 35; DB 6; Length 615; 75.0%; Pred. No. 4.4e+02;
                                     1; Indels
                                     1; Mismatches
                                     6; Conservative
                                                                      1 LKAMDPTP 8
Query Match
Best Local Similarity
Matches 6; Conserv
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|| :|||| 344 LKVVDPTP 351

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Search completed: May 26, 2005, 18:36:58 Job time : 70.8 secs

He A, Au-Young JK, Lee SY; VS, Ison CH, Yang J, Lee EA, Li J) Warren BA, Hafalia AJA, Marquis JP;

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May 26, 2005, 18:43:39; Search time 52.48 Seconds (without alignments) 52.587 Million cell updates/sec
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2. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*
3. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*
3. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*
3. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*
3. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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3. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*
5. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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5. (cgn2_6)ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6. (cgn2_6)ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
6. (cgn2_6)ptodata/1/pubpaa/US60_NEW_PUB.pep:*
6. (cgn2_6)ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1462099 segs, 344972447 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result Query No. Score Match Length DB ID 1 43 100.0 8 14 US-10-047-945-7 2 43 100.0 10 14 US-10-047-945-6 4 3 100.0 12 14 US-10-047-945-6 5 43 100.0 12 14 US-10-047-945-6 6 43 100.0 12 14 US-10-047-945-6 7 35 81.4 30.1 17 US-10-047-945-7 8 100.0 12 14 US-10-047-945-6 8 35 81.4 320 17 US-10-047-945-7 9 35 81.4 320 17 US-10-047-945-7 9 35 81.4 350 17 US-10-732-923-13683 10 35 81.4 359 17 US-10-732-923-13459 11 35 81.4 375 17 US-10-732-923-13459 12 35 81.4 375 17 US-10-732-923-13459 13 35 81.4 375 17 US-10-732-923-13455 14 375 17 US-10-732-923-13455 15 81.4 375 17 US-10-732-923-13455 16 35 81.4 375 17 US-10-732-923-13455 17 US-10-732-923-13455 18 35 81.4 375 17 US-10-732-923-13455 19 35 81.4 375 17 US-10-732-923-13455 10 35 81.4 375 17 US-10-732-923-13455 11 35 81.4 375 17 US-10-732-923-13455 12 35 81.4 375 17 US-10-732-923-13455 13 35 81.4 410 17 US-10-732-923-13463

RESULT 2

Sequence 13464, A		Sequence 13648, A		Sequence 13440, A	н	Sequence 6, Appli	Sequence 17, Appl	Sequence 38, Appl	Sequence 3, Appli					Sequence 20, Appl	Sequence 13441, A	Sequence 63524, A	Sequence 70, Appl	Seguence 5, Appli	Sequence 27, Appl	Sequence 194830,	Sequence 12, Appl	Sequence 284130,	Sequence 253125,	Sequence 151816,	Sequence 13623, A	Sequence 151815,	=	Sequence 6, Appli	-	М	Sequence 13627, A
				7 US-10-732-923-13440		US-09-513-145-6	4 US-10-060-065-17	4 US-10-059-585-38	4 US-10-440-341-3				7 US-10-926-543-90			S US-10-282-122A-63524							5 US-10-424-599-253125			5 US-10-424-599-151815	519	us-1	US-10-732-923-1	US-10-732-92	7 US-10-732-923-13627
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410	41	42	S	602	64	64	648	6	64	648	648	64	648	9	648	o	22	22	22	23	115	ш	۵	17	. 28	31	43	43	63	638	9
81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	79.1	79.1	79.1	79.1	79.1	79.1	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7
32	32	32	32	32	32	35	35	32	32	32	32	32	32	32	32	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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US-10-047-945-7

Sequence 7, Application US/10047945

Sequence 7, Application US/10047945

Publication No. US2003015755A1

GENERAL INFORMATION:

APPLICANT: LIPPS, FREDENICK W.

APPLICANT: LIPPS, FREDENICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

TITLE OF INVENTION: US-10/047,945

CURRENT APPLICATION NUMBER: US/10/047,945

FRICH RETILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US/10/047,945

FRICH RELING DATE:

NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

SEQ ID NO 7

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/FEX:

OCATION:

OCHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above user watches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 1 INFAMIPTE 8

Best Local Similarity 100.0%; Pred. No. 1.30+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 1 LEAMNDFT 8
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Publication No. US2003015755A1;
GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1GE)IMPLICATED DISORDERS
FILE REFREENCE: FWLPATO15US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARR: WORDPERFECT 5.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10047945

Publication No. US2003015755541

GENERAL INFORMATION:
APPLICANT: LIPPS, BINIE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
CURRENT APPLICATION NUMBER: US/10/047,945

PRIOR APPLICATION NUMBER: US/10/047,945

PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 7

SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic.
US-10-047-945-5
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                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LKAMDPTP 8
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US-10-047-945-2
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US-10-047-945-4
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; Sequence 1, Application US/10047945
; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (108) IMPLICATED DISORDERS
; FILE REPERENCE: FWLPATO15US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE:
; FRIOR APPLICATION NUMBER:
; FRIOR APPLICATION NUMBER:
                           Sequence 6, Application US/10047945
Publication No. US20030157555A1
Publication No. US20030157555A1
APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, BRINE V.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E TITLE OF INVENTION: UNABER: US/10/047,945
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR APPLICATION NUMBER:
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Pred. No. 0.16;
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; Pred. No. 1.3e+06;
0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 1
LENGTH: 10
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OTHER INFORMATION: SYNTHESIZED.
OTHER INFORMATION: US 5,576,297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 100.0%;
Similarity 100.0%;
8; Conservative 0;
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US-10-047-945-6
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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US-10-047-945-5
              US-10-047-945-6
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LENGTH: 9
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REPERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
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                                                                                                                            Score 35; DB 17; Length 323;
Pred. No. 1.9e+02;
1; Mismatches 1; Indels
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APPLICANT: BERBER, KTAN
APPLICANT: TRAHIM, PRABHA
APPLICANT: KUMAR, ABHIMAV
APPLICANT: KUMAR, ABHIMAV
APPLICANT: MILBURN, MICHAEL V
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT APPLICATION NUMBER: 60/412,341
PRIOR PILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOSTWARE PALENT ON NUMBER: 60/411,398
SOSTWARE PALENT ON NUMBER: 169
SOSTWARE PALENT ON NUMBER PALENT
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Publication No. US20050108791A1
GENERAL INFORMATION:
            i TYPE: PRT
i ORGANISM: Murine sarcoma virus 3611
US-10-732-923-13460
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 139, Application US/10664421; Publication No. US20040142864A1; GENERAL INFORMATION:
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                                                                                                                                     81.4%;
75.0%;
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Best Local Similarity 75.v.
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Best Local Similarity 75.0
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-10-664-421-139
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52 LKVVDPTP 59
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79 LKVVDPTP 86
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LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2
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; Sequence 13683, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT APPLICATION NUMBER: 10/310,154
; PRIOR PILING DATE: 2002-12-04
; WHOR APPLICATION NUMBER: 10/310,154
; RIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13683
APPLICANT: LIPPS, FREDERICK W.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
TITLE OF INVENTION: (1gg) IMPLICATED DISORDERS
FILE REFERENCE: FWLPATOLSUS
CURRENT APPLICATION NUMBER: US/10/047,945
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Papio hamadryas
US-10-732-923-13683
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                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13465, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING DATE: 2003-128-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2003-128-10
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13465
; LENGTH: 380
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REPRENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: 2003-12-10
PRIOR PEPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13463
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 39 1-15 (52796) C
CURRENT APPLICATION NUMBER: US,10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ. ID NOS: 24149
SEQ ID NO 15529
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.4%; Score 35; DB 17; Length 380; Best Local Similarity 75.0%; Pred. No. 2.2e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 35; DB 17; Length 375; 75.0%; Pred. No. 2.2e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ; ORGANISM: Avian myelocytomatosis virus MH2 US-10-732-923-13465
                                                                                                       Sequence 13529, Application US/10732923
Publication No. US20050108791A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: IC4 retrovirus
US-10-732-923-13529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 LKVVDPTP 112
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88 LKVVDPTP 95
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i Sequence 13464, Application US/10732923

i Publication No. US20050108791A1

i GENERAL INFORMATION.

APPLICANT: Edgercon, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILLS REPERENCE: 38-15(52796)

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

FRIOR FILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-732-923-13646
; Sequence 13646, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REPERENCE: 38-15 (52796)
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; FRIOR PILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13546
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
                                                    Score 35; DB 17; Length 410;
Pred. No. 2.4e+02;
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                                                                                          1; Indels
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                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Avian myelocytomatosis virus MH2
US-10-732-923-13464
ORGANISM: Avian myelocytomatosis virus MH2 US-10-732-923-13463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 26, 2005, 19:18:09 Job time: 73.48 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.4%;
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75.0%;
                                                        81.4%;
75.0%;
                                     Query Match
Best Local Similarity 75...
6; Conservative
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Best Local Similarity 75.v.
6; Conservative
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Best Local Similarity 75...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13646
                                                                                                                                                  || :||||
140 LKVVDPTP 147
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140 LKVVDPTP 147
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                                                                                                                             1 LKAMDPTP 8
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STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SE
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SIP
                                                                                                                                                                                                                                                                                                                                                                                              US-08-657-163A-2
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Appli
Sequence 1, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 5, Appli
                                                                                                         May 26, 2005, 18:29:58 ; Search time 18.24 Seconds (without alignments) 32.741 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*

1: /cgn2_6/ptodateal/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodateal/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodateal/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodateal/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodateal/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodateal/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-310-340A-1

US-08-677-163A-1

US-08-677-163B-42

US-08-571-758-12

US-08-909-984A-12

US-08-909-983-12

US-08-909-983-12

US-08-151-5

US-08-185-282-1

US-08-185-282-1

US-08-185-282-3

US-08-185-282-4

US-08-185-282-4

US-08-185-282-4

US-08-185-282-4

US-08-185-282-4

US-08-185-282-1

US-08-187-282-1

US-08-187-282-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-187-287-1

US-08-171-277-1

US-08-171-277-1

US-08-171-277-1

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US-08-171-277-1
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5-09-574-141A-5
5-09-574-141A-27
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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Match Length DB
                                                                                                                                                                                                          1 LKAMDPTP 8
                                                                                                                                                                                          Perfect score:
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Maximum DB seq
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                                                                                                              Run on:
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No.
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SEQ ID

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Sequence 27, Appli
Sequence 5, Appli
Sequence 27, Appli
Sequence 140, App
Sequence 13211, A
Sequence 3760, Ap
Sequence 3760, Ap
Sequence 5055, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TASAS
COUNTRY: USA
ZIP: 77401
                   US-09-568-189A-5
US-09-568-189A-5
US-09-568-189A-27
US-09-602-777A-140
US-09-949-016-8033
US-09-949-016-8760
US-09-134-000C-3881
US-09-543-681A-5055
US-09-543-681A-5055
US-09-543-681A-5055
US-09-543-681A-22
US-08-247-902A-2
US-08-19-652-6
PCT-US91-09784-4
PCT-US91-09784-4
US-09-949-016-10140
US-09-949-016-10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FABLABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 19 M COMPATIBLE
OMPHOTER: 19 M COMPATIBLE
OMPRATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFTCATION DATA:
APPLICATION WUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFTCATION: 514
PRIOR DATE: 12 SEPTEMBER 1994
CLASSIFTCATION: 514
APPLICATION NUMBER: 08/310,340
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
REGISTRATION NUMBER: 28,198
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
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ANTI-SENSE: NO FRAGMENT TYPE: N ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BELLAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                JOURNAL:
VOLUME:
VOLUME:
VOLUME:
ISSUE: PI
                                                                                                                                                                    US-08-310-340A-1
                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-657-163A-1
                   TITLE: A
 AUTHORS:
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                                                                                                                                                                                                                                 Sequence 1, Application US/08310340A
Patent No. 5576297
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                   ö
                                                                                     Gaps
                                                                                     ö
                                                100.0%; Score 43; DB 1; Length 10; 100.0%; Pred. No. 0.018;
                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
CRANELINE:
ORGANIZINE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEPAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: ADULT
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
ORIGINAL SOURCE: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: DIDELPHIS
STRAIN: WILD
INDIVIDUAL ISOLATE:
                                                                                                                                          1 LKAMDPTP 8
                                                                                                                     1 LKAMDPTP
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      US-08-657-163A-2
                                                                                                                                                                                                                        US-08-310-340A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Gaps
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APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LINES AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF EQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 43; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 0.028; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                 10TH WORLD CONGRESS ON ANIMAL
PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
SINGAPORE
PROGRAMME AND ABSTRACTS
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ORGANISM: DIDELPHIS VIRGINIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
: JONAS PERALES, ET AL.
ANTI-SYMBE VENOM FORM DIDELPHIDAE
.: INTERNATIONAL SOCIETY ON
TOXINOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION S14
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTONEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
RESTERNEE/DOCKET NUMBER: FWL-PATTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID
UVDOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08657163A Patent No. 5744449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 713-482-296
TELEFAX: 713-663-7290
TELEX:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                               3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                1 LKAMDPTP 8
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Hanks, S. K.
Quinn, A. M.
                                                                                                        ZIP: 94104
                                                            TITLE: Th
JOURNAL:
VOLUME: 2
                                                                                                                                                             US-07-857-224B-42
    AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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CUNTRY: Switzerland
ZIP: none
ZIP: (note: this is an international post code) CH-8092
ZIP: (note: this is an international post code) CM-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacCintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIPICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
                                                                                                                                                                                                                                 AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 43; DB 1; Length 15; 100.0%; Pred. No. 0.028; tive 0; Mismatches 0; Indels
                                                                                                                                     ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
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FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/07857224B
Patent No. 5958784
                      TEXAS WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                             CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES
TITLE: ANTI-SNAKE VENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
STRAIN: WILD
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                        HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                            3-8 NOV 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LKAMDPTP 8
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                                                                                                                                                                                                                                                                                                                                                                          PAGES: 104
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Patent No. 5700675
GENERAL INPORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Therrien, Marc
APPLICANT: Karim, Pelix D.
APPLICANT: Massarman, David A.
TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 2
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                 Gaps
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                                                                                                                                                     Score 35; DB 2; Length 267; Pred. No. 28; 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 34;
1; Mismatches
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CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 75.0%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
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: USA
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STRANDEDNESS: no
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1 LKAMDPTP 8
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Best Local Similarity
Matches 6; Conserv
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Sequence 12, Application:

APPLICANT: Rubin, Gerry M.

APPLICANT: Karim, Felix D.

APPLICANT: Wassarman, David A.

TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras

TITLE OF INVENTION: Signal Transduction

NUMBER OF SEQUENCE: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200
       Sequence 12, Application US/08909984A

Patent No. 5747275

GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Karim, Felix D.
APPLICANT: Wassarman, David A.
TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras TITLE OF INVENTION: Signal Transduction
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                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STRATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (515) 343-4341
TELEFAX: (515) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 315 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLGGY: not relevant
MOLECULE TYPE: peptide
US-08-909-984A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0°
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CITY: SAN FRANCISCO
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US-08-909-984A-12
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                                                                                                                                                                                                                                                                       Length 648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rapp, Ulf R.
APPLICANT: Storm, Stephen M.
TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1;
Pred. No. 75;
1; Mismatches
                                                                                                                                                                                                                                                                     Score 35; DB 1;
Pred. No. 75;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
FILORASIFICATION DATA:
PRILICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFRENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
   NAME: Torchia, Ph.D., Timothy E
REGISTRATION NUMBER: 36,700
REPERENCE/DOCKET NUMBER: 0NYX-005/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5481
TELEPAX: (415) 857-0663
INFORMATION FOR SECIED 1000: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1615 L Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-185-282-1; Sequence 1, Application US/08185282; Patent No. 5618670; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       81.4%;
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75.0%;
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 648 amino acids TYPE: amino acid
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Best Local Similarity 75.v
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                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-151-2
                                                                                                                                                                                                                                                                                                                                                                                     377 LKVVDPTP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 LKVVDPTP 384
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Best Local Similarity
Local 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                  1 LKAMDPTP
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Factor No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09489, 039A
CURRENT APPLICATION NUMBER: US/09489, 039A
CURRENT FILING DATE: 1090-01-27
PRIOR PELICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9126
LENGTH: 405
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Patent No. 559719
GENERAL INFORMATION:
APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCES:
ADDRESSEE: Cooley Godward et al.
STREET: Five Palo Alto
CITY: Palo Alto
                                                                                                                                                                        81.4%; Score 35; DB 1; Length 346; 75.0%; Pred. No. 37; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 35; DB 4; Length 405; 75.0%; Pred. No. 44; ive 1; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,151
FILING DATE: 14-JUL-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Klebsiella pneumoniae
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRACMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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186 IKARDPTP 193
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75 LKVVDPTP 82
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US-08-276-151-5
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PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 861-3000
TELEFRAX: (202) 861-300
TELEFRAX: (202) 861-300
TELEFRAX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
PATLING DATE:
CLASSIFICATION 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82
TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
TELEFAX: 6714627 CUSH
TELERAX: 6714627 CUSH
TELERAX: 6714627 CUSH
TELERAX: 6714627 CUSH
TELEX: 6714627 CUSH
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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- 377 LKVVDPTP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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Sequence 2, Application US/08185282

Sequence 2, Application US/08185282

Patent No. 5618670

GENERAL INFORMATION:

APPLICANT: Storm, Stephen M.

TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES

TUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHWAN, DARBY & CUSHWAN

STREET: 1615 L Street, N.W.

CITY: Washington.

STATE: D.C.

COUNTRY: USA

IP OF COUNTRY: USA

COUNTRY: USA

D.C.

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: USA

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/185, 282
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| Patent No. 5618670
| GENERAL INFORMATION:
| APPLICANT: Rapp, Ulf R. APPLICANT: Storm, Stephen M. TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES INVERSPONDENCES: 12
| CORRESPONDENCES: 12
| CORRESPONDENCES: 12
| CITY: Washington STREET: 161E Street, N.W. STREET: 161E Street, N.W. STATE: D.C. COUNTRY: USA
| STATE: D.C. COUNTRY: USA
| COMPUTER: PLOSMS | COMPUTER: PLOSMS | COMPUTER: PLOSMS | COMPUTER: IBM PC Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SCOCT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 26,581
TELECOMMUNICATION INFORMATION:
TELEPA: (202) 861-3000
TELEFA: (202) 862-0944
TELEX: (714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION BATA:
APPLICATION NUMBER: US/07/759,738
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SCOLT, WALSON T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 648 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-185-282-2
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Gaps
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US-08-185-282-4
; Sequence 4, Application US/08185282
; Sequence 7, Application US/08185282
; CENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.;
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; Length 648;
Pred. No. 75;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,282
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; Sequence 5, Application US/08185282
; Retent No. 5618670
; GENERAL INFORMATION:
    APPLICANT: Rapp, Ulf R.
    TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS: 12
    CORRESPONDENCE ADDRESS: 14
    STREET: 1615 L Street, N.W.
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20036-5601
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: PREADABLE FORM:
    MEDIUM TYPE: PLOS/MS-DOS
    SOFFWARE: PREADABLE FORM:
    COMPUTER: PREADABLE FORM:
    MEDIUM TREE: PREADABLE FORM:
    COMPUTER: PREADABLE FORM:
    MEDIUM TREE: PREADABLE FORM:
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                                                                                                                      Query Match 81.4%; Score 35; DB 1; Length 648; Best Local Similarity 75.0%; Pred. No. 75; Matches 6; Conservative 1; Mismatches 1; Indels
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/759,738
FILLING DATE:
ATTORNEY AGENT INFORMATION:
NAME: SCOCT, WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 861-3000
TELEFAX: (202) 82-0944
TELEFAX: (202) 82-0944
TELEFAX: G714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
US-08-185-282-5
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                       1 LKAMDPTP 8
; TOPOLOGY: linear
US-08-185-282-4
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US-08-185-282-5
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Search completed: May 26, 2005, 19:08:41 Job time : 19.44 secs

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